IN THE UNITED STATES PATENT & TRADEMARK OFFICE

In re Application	:	Mats Hellstrom et al.
Serial No.	:	10/581,761
Filed	:	June 5, 2006
For	:	AngioGenetics Sweden AB
Examiner	:	
Attorney Docket	:	102959-202
Group Art Unit	:	1653
Confirmation No.	:	6588
Customer No.	:	27267

* *

I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: Mail Stop PCT, Commissioner for Patents, P. O. Box 1450, Alexandria, Virginia 22313-1450 on 08 APR 2008, 2008.

By Todd E. Garabedian
Todd E. Garabedian, Ph.D.
Registration No. 39,197
Attorney for Applicants

* *

Attention: PCT Legal Staff
Mail Stop PCT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

RESPONSE TO NOTIFICATION OF MISSING REQUIREMENTS FILED WITH A PETITION UNDER 37 CFR §1.137(b)

Dear Sir:

As part of the enclosed Petition to Revive under 37 CFR §1.137(b), and with respect to the Notification of Missing Requirements Under 35 USC §371 mailed February 13, 2007, Applicants submit herewith a signed Combined Declaration and

Power of Attorney for Joint Inventors relating to the above-identified non-provisional patent application.

In addition, a copy of the sequence listing in computer-readable form (CRF) is submitted herewith as also requested in the enclosed notice. A duplicate copy of the written sequence listing as submitted to the USPTO on June 5, 2006 is enclosed. Applicants herein request the sequence listing be entered into the above-identified application.

Applicants state that with regard to the Sequence Listing, the information recorded in computer readable form is identical to the written sequence listing. Applicants submit no new matter is added herewith.

Please charge the surcharge of $130.00 for filing the Declaration to Deposit Account No. 23-1665 as well as any other fees due with respect to this Response.

An additional copy of this Transmittal Letter is enclosed along with a copy of the Notification to File Missing Requirements.

04/11/2008 GFREY1 00000046 231565 10581761
01 FC:1617 130.00 DA

If the Examiner believes a telephone conference would aid in the continued prosecution of this application, the Examiner is invited and encouraged to contact Applicants' representative at the telephone number listed below.

Respectfully submitted,

Mats Hellstrom et al.

Date: 08 APR 2008

By Todd E. Garabedian

Todd E. Garabedian, Ph.D.
Registration No. 39,197
Attorney for Applicants

WIGGIN AND DANA LLP
One Century Tower
New Haven, CT 06508
Telephone: (203) 498-4400
Fax: (203) 782-2889

\18516\10\58905.1

PTO/SB/64/PCT (05-07)
Approved for use through 02/28/2010. OMB 0651-0021
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

PETITION FOR REVIVAL OF AN INTERNATIONAL APPLICATION FOR PATENT DESIGNATING THE U.S. ABANDONED UNINTENTIONALLY UNDER 37 CFR 1.137(b)

Docket Number (Optional): 102959-202

First Named Inventor: Mats Hellstrom

International (PCT) Application No.: PCT/SE04/01814

U.S. Application No.: 10/581,761 (if known)

Filed: June 5, 2006

Title: Angiogenesis affecting polypeptides, proteins, and composition, and methods of use thereof

Attention: PCT Legal Staff
Mail Stop PCT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

The above-identified application became abandoned as to the United States because the fees and documents required by 35 U.S.C. 371(c) were not filed prior to the expiration of the time set in 37 CFR 1.495(b) or (c) as applicable. The date of abandonment is the day after the date on which the 35 U.S.C. 371(c) requirements were due. See 37 CFR 1.495(h).

APPLICANT HEREBY PETITIONS FOR REVIVAL OF THIS APPLICATION

NOTE: A grantable petition requires the following items:
(1) Petition fee
(2) Proper reply
(3) Terminal disclaimer with disclaimer fee which is required for all international applications having an international filing date before June 8, 1995; and
(4) Statement that the entire delay was unintentional.

1. Petition fee

☐ Small entity - fee $_____(37 CFR 1.17(m)). Applicant claims small entity status. See 37 CFR 1.27.

☒ Other than small entity - fee $ 1,500.00 (37 CFR 1.17(m))

2. Proper reply

A. The proper reply (the missing 35 U.S.C. 371(c) requirement(s)) in the form of a Declaration and computer readable sequence listing CD (identify type of reply):

☐ has been filed previously on _____.

☒ is enclosed herewith.

04/11/2008 GFREY1 00000048 231665 10581761

02 FC:1453 1540.00 DA

3. Terminal disclaimer with disclaimer fee

[X] Since this international application has an international filing date on or after June 8, 1995, no terminal disclaimer is required.

[ ] A terminal disclaimer (and disclaimer fee (37 CFR 1.20(d)) of $ _____ for a small entity or $_____ for other than a small entity) disclaiming the required period of time is enclosed herewith (see PTO/SB/63).

4. Statement. The entire delay in filing the required reply from the due date for the required reply until the filing of a grantable petition under 37 CFR 1.137(b) was unintentional.

WARNING:

Petitioner/applicant is cautioned to avoid submitting personal information in documents filed in a patent application that may contribute to identity theft. Personal information such as social security numbers, bank account numbers, or credit card numbers (other than a check or credit card authorization form PTO-2038 submitted for payment purposes) is never required by the USPTO to support a petition or an application. If this type of personal information is included in documents submitted to the USPTO, petitioners/applicants should consider redacting such personal information from the documents before submitting them to the USPTO. Petitioner/applicant is advised that the record of a patent application is available to the public after publication of the application (unless a non-publication request in compliance with 37 CFR 1.213(a) is made in the application) or issuance of a patent. Furthermore, the record from an abandoned application may also be available to the public if the application is referenced in a published application or an issued patent (see 37 CFR 1.14). Checks and credit card authorization forms PTO-2038 submitted for payment purposes are not retained in the application file and therefore are not publicly available.

Todd E. Garabedian

Signature

08 APR 2008

Date

Todd E. Garabedian, Ph.D.

Typed or Printed Name

39,197

Registration Number, if applicable

Wiggin and Dana LLP, One Century Tower. P.O. Box 1832

Address

(203) 498-4400

Telephone Number

New Haven, CT 06508-1832

Address

Enclosures: [X] Response

[X] Fee Payment

[ ] Terminal Disclaimer

[X] Other (please identify): Declaration

Sequence listing in computer readable form (CD)

Written sequence listing

Notification of Missing Requirements

PTO/SB/64/PCT (05-07)
Approved for use through 02/28/2010. OMB 0651-0021
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

PETITION FOR REVIVAL OF AN INTERNATIONAL APPLICATION FOR PATENT DESIGNATING THE U.S. ABANDONED UNINTENTIONALLY UNDER 37 CFR 1.137(b)

Docket Number (Optional): 102959-202

First Named Inventor: Mats Hellstrom

International (PCT) Application No.: PCT/SE04/01814

U.S. Application No.: 10/581,761 (if known)

Filed: June 5, 2006

Title: Angiogenesis affecting polypeptides, proteins, and composition, and methods of use thereof

Attention: PCT Legal Staff
Mail Stop PCT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

The above-identified application became abandoned as to the United States because the fees and documents required by 35 U.S.C. 371(c) were not filed prior to the expiration of the time set in 37 CFR 1.495(b) or (c) as applicable. The date of abandonment is the day after the date on which the 35 U.S.C. 371(c) requirements were due. See 37 CFR 1.495(h).

APPLICANT HEREBY PETITIONS FOR REVIVAL OF THIS APPLICATION

NOTE: A grantable petition requires the following items:
(1) Petition fee
(2) Proper reply
(3) Terminal disclaimer with disclaimer fee which is required for all international applications having an international filing date before June 8, 1995; and
(4) Statement that the entire delay was unintentional.

1. Petition fee

☐ Small entity - fee $_____(37 CFR 1.17(m)). Applicant claims small entity status. See 37 CFR 1.27.

☒ Other than small entity - fee $ 1,500.00 (37 CFR 1.17(m))

2. Proper reply

A. The proper reply (the missing 35 U.S.C. 371(c) requirement(s)) in the form of a Declaration and computer readable sequence listing CD (identify type of reply):

☐ has been filed previously on _____.

☒ is enclosed herewith.

3. Terminal disclaimer with disclaimer fee

[X] Since this international application has an international filing date on or after June 8, 1995, no terminal disclaimer is required.

[ ] A terminal disclaimer (and disclaimer fee (37 CFR 1.20(d)) of $ _____ for a small entity or $_____ for other than a small entity) disclaiming the required period of time is enclosed herewith (see PTO/SB/63).

4. Statement. The entire delay in filing the required reply from the due date for the required reply until the filing of a grantable petition under 37 CFR 1.137(b) was unintentional.

WARNING:

Petitioner/applicant is cautioned to avoid submitting personal information in documents filed in a patent application that may contribute to identity theft. Personal information such as social security numbers, bank account numbers, or credit card numbers (other than a check or credit card authorization form PTO-2038 submitted for payment purposes) is never required by the USPTO to support a petition or an application. If this type of personal information is included in documents submitted to the USPTO, petitioners/applicants should consider redacting such personal information from the documents before submitting them to the USPTO. Petitioner/applicant is advised that the record of a patent application is available to the public after publication of the application (unless a non-publication request in compliance with 37 CFR 1.213(a) is made in the application) or issuance of a patent. Furthermore, the record from an abandoned application may also be available to the public if the application is referenced in a published application or an issued patent (see 37 CFR 1.14). Checks and credit card authorization forms PTO-2038 submitted for payment purposes are not retained in the application file and therefore are not publicly available.

Todd E. Garabedian

Signature

08 APR 2008

Date

Todd E. Garabedian, Ph.D.

Typed or Printed Name

39,197

Registration Number, if applicable

Wiggin and Dana LLP, One Century Tower, P.O. Box 1832

Address

(203) 498-4400

Telephone Number

New Haven, CT 06508-1832

Address

Enclosures:
[X] Response
[X] Fee Payment
[ ] Terminal Disclaimer
[X] Other (please identify): Declaration
Sequence listing in computer readable form (CD)
Written sequence listing
Notification of Missing Requirements

PTO/SB/17 (10-07)
Approved for use through 06/30/2010. OMB 0651-0032
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE
Under the Paperwork Reduction Act of 1995 no persons are required to respond to a collection of information unless it displays a valid OMB control number

Effective on 12/08/2004.
Fees pursuant to the Consolidated Appropriations Act, 2005 (H.R. 4818).

FEE TRANSMITTAL
For FY 2008

☐ Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT ($)

Complete if Known	
Application Number	10/581,761
Filing Date	June 5, 2006
First Named Inventor	Mats Hellstrom
Examiner Name	
Art Unit	1653
Attorney Docket No.	102959-202

METHOD OF PAYMENT (check all that apply)

☐ Check ☐ Credit Card ☐ Money Order ☐ None ☐ Other (please identify): _____

☑ Deposit Account Deposit Account Number: 23-1665 Deposit Account Name: _____

For the above-identified deposit account, the Director is hereby authorized to: (check all that apply)

☑ Charge fee(s) indicated below ☐ Charge fee(s) indicated below, **except for the filing fee**

☑ Charge any additional fee(s) or underpayments of fee(s) under 37 CFR 1.16 and 1.17 ☑ Credit any overpayments

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

FEE CALCULATION

1. BASIC FILING, SEARCH, AND EXAMINATION FEES

Application Type	FILING FEES Fee ($)	FILING FEES Small Entity Fee ($)	SEARCH FEES Fee ($)	SEARCH FEES Small Entity Fee ($)	EXAMINATION FEES Fee ($)	EXAMINATION FEES Small Entity Fee ($)	Fees Paid ($)
Utility	310	155	510	255	210	105	
Design	210	105	100	50	130	65	
Plant	210	105	310	155	160	80	
Reissue	310	155	510	255	620	310	
Provisional	210	105	0	0	0	0	

2. EXCESS CLAIM FEES

Fee Description	Fee ($)	Small Entity Fee ($)
Each claim over 20 (including Reissues)	50	25
Each independent claim over 3 (including Reissues)	210	105
Multiple dependent claims	370	185

Total Claims	Extra Claims	Fee ($)	Fee Paid ($)
_____ - 20 or HP =	_____	x _____	= _____

HP = highest number of total claims paid for, if greater than 20.

Indep. Claims	Extra Claims	Fee ($)	Fee Paid ($)
_____ - 3 or HP =	_____	x _____	= _____

HP = highest number of independent claims paid for, if greater than 3.

Multiple Dependent Claims Fee ($)	Multiple Dependent Claims Fee Paid ($)
_____	_____

3. APPLICATION SIZE FEE

If the specification and drawings exceed 100 sheets of paper (excluding electronically filed sequence or computer listings under 37 CFR 1.52(e)), the application size fee due is $260 ($130 for small entity) for each additional 50 sheets or fraction thereof. See 35 U.S.C. 41(a)(1)(G) and 37 CFR 1.16(s).

Total Sheets	Extra Sheets	Number of each additional 50 or fraction thereof	Fee ($)	Fee Paid ($)
_____ - 100 =	_____ / 50 =	_____ (round **up** to a whole number)	x _____	= _____

4. OTHER FEE(S)

	Fees Paid ($)
Non-English Specification, $130 fee (no small entity discount)	_____
Other (e.g., late filing surcharge): Petition Fee for Revival of an Application	$1500.00

SUBMITTED BY

Signature	Todd E. Garabedian	Registration No. (Attorney/Agent) 39,197	Telephone 203-498-4400
Name (Print/Type)	Todd E. Garabedian, Ph.D.		Date 08 APR 2008

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/581,761	Mats Hellstrom	020876419PCTUS

INTERNATIONAL APPLICATION NO.	
PCT/SE04/01814	
I.A. FILING DATE	PRIORITY DATE
12/06/2004	12/05/2003

23432
COOPER & DUNHAM, LLP
1185 AVENUE OF THE AMERICAS
NEW YORK, NY 10036

CONFIRMATION NO. 6588

371 FORMALITIES LETTER

OC000000022476482

Date Mailed: 02/13/2007

NOTIFICATION OF MISSING REQUIREMENTS UNDER 35 U.S.C. 371 IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

The following items have been submitted by the applicant or the IB to the United States Patent and Trademark Office as a Designated / Elected Office (37 CFR 1.495).

- Copy of the International Application filed on 06/05/2006
- Copy of the International Search Report filed on 06/05/2006
- Preliminary Amendments filed on 06/05/2006
- Biochemical Sequence Listing filed on 06/05/2006
- U.S. Basic National Fees filed on 06/05/2006
- Priority Documents filed on 06/05/2006
- Specification filed on 06/05/2006
- Claims filed on 06/05/2006
- Abstracts filed on 06/05/2006
- Drawings filed on 06/05/2006

The following items **MUST** be furnished within the period set forth below in order to complete the requirements for acceptance under 35 U.S.C. 371:

- Oath or declaration of the inventors, in compliance with 37 CFR 1.497(a) and (b), identifying the application by the International application number and international filing date.

- A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e). If the effective filing date is on or after September 8, 2000, see the final rulemaking notice published in the Federal Register at 65 FR 54604 (September 8, 2000) and 1238 OG 145 (September 19, 2000). Applicant must provide an initial computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). If applicant desires the sequence listing in the instant application to be identical with that of another application on file in the U.S. Patent and Trademark Office, such request in accordance with 37 CFR 1.821(e) may be submitted in lieu

of a new CRF.

ALL OF THE ITEMS SET FORTH ABOVE MUST BE SUBMITTED WITHIN TWO (2) MONTHS FROM THE DATE OF THIS NOTICE OR BY 32 MONTHS FROM THE PRIORITY DATE FOR THE APPLICATION, WHICHEVER IS LATER. FAILURE TO PROPERLY RESPOND WILL RESULT IN ABANDONMENT.

The time period set above may be extended by filing a petition and fee for extension of time under the provisions of 37 CFR 1.136(a).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- **For Rules Interpretation, call (571) 272-0951**
- **For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.**
- **Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov**

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.
https://sportal.uspto.gov/authenticate/AuthenticateUserLocalEPF.html

For more information about EFS-Web please call the USPTO Electronic Business Center at **1-866-217-9197** or visit our website at http://www.uspto.gov/ebc.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

DEBORAH D WILLIAMS

Telephone: (703) 308-9140 EXT 205

PART 2 - OFFICE COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/581,761	PCT/SE04/01814	020876419PCTUS

FORM PCT/DO/EO/905 (371 Formalities Notice)

069625-081517

Docket No: 102959-202

COMBINED DECLARATION AND POWER OF ATTORNEY FOR JOINT INVENTORS

1. As below named joint inventors, we hereby declare that our addresses and citizenship are as stated below next to our names. We believe we are the original and first inventors of the subject matter which is claimed and for which a patent is sought on the invention entitled:

ANGIOGENESIS AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS, AND METHODS OF USE THEREOF

the specification of which:

[ ] is attached or

[X] was filed on June 5, 2006 as Serial No. 10/581,761.

2. We hereby state that we have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment specifically referred to above.

3. We acknowledge the duty to disclose information which is material to patentability as defined in 37 C.F.R. 1.56.

4. [X] We hereby claim foreign priority benefits under Title 35, United States Code, §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate or §365(a) of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by us on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

Country	Application Serial No.	Date of Filing (day, mo., yr.)	Priority Claimed under 35 U.S.C. § 119	
Sweden	0303268-7	December 5, 2003	[X] Yes	[ ] No
			[ ] Yes	[ ] No
			[ ] Yes	[ ] No

5. [X] We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s), § 365(c) of any PCT international application designating the United States of America, and § 119(e) of any United States provisional application(s) that is/are listed below and, insofar as the subject matter of each of the claims of this

069625-081517

application is not disclosed in that/those prior application(s) in the manner provided by the first paragraph of Title 35, United States Code, § 112, we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application(s) and the filing date of this application:

Application Serial No.	Filing Date	Status
60/481,741	December 5, 2003	Pending
PCT/SE2004/001814	December 6, 2004	Pending

6. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

7. As named inventor, I hereby appoint the attorneys of **Wiggin and Dana LLP, Customer Number 27267**, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

8. Please send all correspondence to:

Docket Coordinator
Intellectual Property Law Section
Wiggin and Dana LLP
One Century Tower
P. O. Box 1832
New Haven, Connecticut 06508-1832
Telephone: (203) 498-4400

Customer No:

27267

9. [X] As named inventors, we hereby appoint the attorneys listed in paragraph 7 as our domestic representatives for the invention identified in paragraph 1 with full power of substitution and revocation, to transact all business in the U.S. Patent and Trademark Office and in the U.S. courts in connection therewith. They also designated as domestic representative on whom process or notice of proceedings affecting the application or patents issuing therefrom may be served.

[X] We hereby authorize the U. S. attorneys named in paragraph 7 to accept and follow instruction from Albihns AB as to any actions to be taken in the U.S. Patent and Trademark Office regarding this application without direct

069625-081517

communication between the U.S. attorneys and us. In the event of a change in the persons from whom instructions may be taken, we will notify the U.S. attorneys.

10. Inventor Information:

Full name of **first** inventor: Mats HELLSTRÖM
Inventor's Signature:
Date: 26 February 2008 Citizenship: Sweden
Residence: Ymergatan 15B, SE-753 25 Uppsala, Sweden
Post Office Address: Ymergatan 15B, SE-753 25 Uppsala, Sweden

Full name of **second** inventor: Elisabet WALLGARD
Inventor's Signature:
Date: 27 FEBRUARY 2008 Citizenship: Sweden
Residence: c/o Kerstin Wallgard, Stjärnstigen 17, SE-561 35 Huskvarna, Sweden
Post Office Address: c/o Kerstin Wallgard, Stjärnstigen 17, SE-561 35 Huskvarna, Sweden

Full name of **third** inventor: Mattias KALÉN
Inventor's Signature:
Date: 26 FeS 2008 Citizenship: Sweden
Residence: Larsbergsvägen 19, SE-181 38 Lidingö, Sweden
Post Office Address: Larsbergsvägen 19, SE-181 38 Lidingö, Sweden

This is the end of the listing of inventors.

\18516\10\55362.1

SEQUENCE LISTING

<110> Hellström, Mats
Wallgard, Elisabet
Kalén, Mattias

<120> ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS, AND METHODS OF USE THEREOF

<130> 78063

<160> 52

<170> PatentIn version 3.2

<210> 1
<211> 736
<212> DNA
<213> Murinae gen. sp.

<400> 1
gtgatccagg atccgaagag gcccggagca ggagcatggc gtcgtcgggg tcggtgcagc 60

agctgcccct ggtgctgctg atgttgctgt tggcgagtgc ggcacgggcc agactctact 120

tccgctcggg ccagacttgc taccatccca ttcgcgggga ccagctggct ctgctggggc 180

gcaggactta tcctcggccg catgagtacc tgtccccagc ggatctcccc aagaattggg 240

actggagaaa tgtgaacggt gtcaactatg ccagcgtcac caggaaccag cacatcccac 300

agtactgtgg ttcctgctgg gcccacggca gcaccagtgc catggcagac cgaatcaaca 360

tcaagaggaa aggtgcatgg ccctccatcc tgctgtccgt acagaatgtc attgactgtg 420

gcaatgctgg ctcttgtgaa gggggcaatg accttccggt gtgggagtat gcccacaagc 480

atggcatccc cgatgagacc tgcaacaact accaggcaag gaccaagact gtgacaagtt 540

taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga attacaccct 600

ctggagagtg ggtgattacg gtccctgtcc gggagggaga agatgatggc gagatctatg 660

ccaatggtcc catcagctgc gggataatgg gcaccagaga tgatgtctaa ctacactggg 720

ggcatctatg ctgagc 736

<210> 2
<211> 1404
<212> DNA
<213> Murinae gen. sp.

<400> 2
aaaggaccgg gcggggcgtc ccgagcgcgt gggcctgcgg gtcgggtcaa gaggtcgaag 60

gtgctgcgcg tgatccagga tccgaattgg cccggagcag gagcatggcg tcgtcggggt 120

cggtgcagca gctgcccctg gtgctgctga tgttgctgtt ggcgagtgcg gcacgggcca 180

gactctactt ccgctcgggc cagacttgct accatcccat tcgcggggac cagctggctc 240

tgctggggcg caggacttat cctcggccgc atgagtacct gtccccagcg gatctcccca 300

agaattggga ctggagaaat gtgaacggtg tcaactatgc cagcgtcacc aggaaccagc 360

acatcccaca gtactgtggt tcctgctggg cccacggcag caccagtgcc atggcagacc 420

gaatcaacat caagaggaaa ggtgcatggc cctccatcct gctgtccgta cagaatgtca 480

ttgactgtgg caatgctggc tcttgtgaag ggggcaatga ccttccggtg tgggagtatg 540

cccacaagca tggcatcccc gatgagacct gcaacaacta ccaggccaag gaccaagact 600

gtgacaagtt taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga 660

attacaccct ctggagagtg ggtgattacg gctccctgtc cgggagggag aagatgatgg 720

ccgagatcta tgccaatggt cccatcagct gcgggataat ggcaacagag atgatgtcta 780

actacactgg gggcatctat gctgagcacc aggaccaggc cgttatcaac cacatcatct 840

ctgtagctgg ctggggtgtc agcaacgatg gcatcgagta ctggattgtc cgaaattcat 900

ggggcgaacc ctggggtgag aaaggctgga tgaggatcgt gaccagcacc tacaagggag 960

gcacaggtga cagctacaac cttgccatcg agagtgcctg cacatttggg gaccccattg 1020

tttaggtaga tgtctctgga agcagcgctg tgaaccatga cagggagggg tgattaatta 1080

ctgacactgg acatgtccag acagctataa acagtgcttg tggacatgag gaccagagtg 1140

tggactgcat cccgagagga gacggtaaag gatgaaacac aactgcactg ggaccctccg 1200

ccgtaccctc caggcctgcc tcctccacca ctgagccctc caggcctgcc tcctcttcta 1260

cagtgcttgc cttcagccac ccggagaaga gagctatggt ttaggacagc tcaacttatc 1320

accagatctg gagccctgga atccatggga ggggggaaca agtccagact gcttaagaaa 1380

tgagtaaaat atctggcttc ccac 1404

<210> 3
<211> 306
<212> PRT
<213> Murinae gen. sp.

<400> 3

Met Ala Ser Ser Gly Ser Val Gln Gln Leu Pro Leu Val Leu Leu Met
1 5 10 15

Leu Leu Leu Ala Ser Ala Ala Arg Ala Arg Leu Tyr Phe Arg Ser Gly
20 25 30

Gln Thr Cys Tyr His Pro Ile Arg Gly Asp Gln Leu Ala Leu Leu Gly
35 40 45

Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu
50 55 60

```
Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser
65                  70                  75                  80

Val Thr Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala
                85                  90                  95

His Gly Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys
            100                 105                 110

Gly Ala Trp Pro Ser Ile Leu Leu Ser Val Gln Asn Val Ile Asp Cys
        115                 120                 125

Gly Asn Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Pro Val Trp Glu
    130                 135                 140

Tyr Ala His Lys His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln
145                 150                 155                 160

Ala Lys Asp Gln Asp Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Thr
                165                 170                 175

Glu Phe Lys Glu Cys His Thr Ile Gln Asn Tyr Thr Leu Trp Arg Val
            180                 185                 190

Gly Asp Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile
        195                 200                 205

Tyr Ala Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Met Met
    210                 215                 220

Ser Asn Tyr Thr Gly Gly Ile Tyr Ala Glu His Gln Asp Gln Ala Val
225                 230                 235                 240

Ile Asn His Ile Ile Ser Val Ala Gly Trp Gly Val Ser Asn Asp Gly
                245                 250                 255

Ile Glu Tyr Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu
            260                 265                 270

Lys Gly Trp Met Arg Ile Val Thr Ser Thr Tyr Lys Gly Gly Thr Gly
        275                 280                 285

Asp Ser Tyr Asn Leu Ala Ile Glu Ser Ala Cys Thr Phe Gly Asp Pro
    290                 295                 300

Ile Val
305
```

<210> 4
<211> 1480
<212> DNA
<213> Homo sapiens

<400> 4
ctgggccgag gccgaggccg gggcgggatc cagagcggga gccggcgcgg gatctgggac 60

tcggagcggg atccggagcg ggacccagga gccggcgcgg ggccatggcg aggcgcgggc 120

cagggtggcg gccgcttctg ctgctcgtgc tgctggcggg cgcggcgcag ggcggcctct 180

acttccgccg gggacagacc tgctaccggc ctctgcgggg ggacgggctg gctccgctgg 240

ggcgcagcac atacccccgg cctcatgagt acctgtcccc agcggatctg cccaagagct 300

gggactggcg caatgtggat ggtgtcaact atgccagcat cacccggaac cagcacatcc 360

cccaatactg cggctcctgc tgggcccacg ccagcaccag cgctatggcg gatcggatca 420

acatcaagag gaagggagcg tggccctcca ccctcctgtc cgtgcagaac gtcatcgact 480

gcggtaacgc tggctcctgt gaaggggtga atgacctgtc cgtgtgggac tacgcccacc 540

agcacggcat ccctgacgag acctgcaaca actaccaggc caaggaccag gagtgtgaca 600

agtttaacca atgtgggaca tgcaatgaat tcaaagagtg ccacgccatc cggaactaca 660

ccctctggag ggtgggagac tacggctccc tctctgggag ggagaagatg atggcagaaa 720

tctatgcaaa tggtcccatc agctgtggaa taatggcaac agaaagactg gctaactaca 780

ccggaggcat ctatgccgaa taccaggaca ccacatatat aaaccatgtc gtttctgtgg 840

ctgggtgggg catcagtgat gggactgagt actggattgt ccggaattca tggggtgaac 900

catggggcga gagaggctgg ctgaggatcg tgaccagcac ctataaggat gggaagggcg 960

ccagatacaa ccttgccatc gaggagcact gtacatttgg ggaccccatc gtttaaggcc 1020

atgtcactag aagcgcagtt taagaaaagg catggtgacc catgaccaga ggggatccta 1080

tggttatgtg tgccaggctg gctggcagga actggggtgg ctatcaatat tggatggcga 1140

ggacagcgtg gcactggctg cgagtgttcc tgagagttga aagtgggatg acttatgaca 1200

cttgcacagc atggctctgc ctcacaatga tgcagtcagc cacctggtga agaagtgacc 1260

tgcgacacag gaaacgatgg gacctcagtc ttcttcagca gaggacttga tattttgtat 1320

ttggcaactg tgggcaataa tatggcattt aagaggtgaa agagttcaga cttatcacca 1380

ttcttatgtc actttagaat caagggtggg ggagggaggg agggagttgg cagtttcaaa 1440

tcgcccaagt gatgaataaa gtatctggct ctgcacgaga 1480

<210> 5
<211> 303
<212> PRT
<213> Homo sapiens

<400> 5

```
Met Ala Arg Arg Gly Pro Gly Trp Arg Pro Leu Leu Leu Leu Val Leu
1               5                  10                  15

Leu Ala Gly Ala Ala Gln Gly Gly Leu Tyr Phe Arg Arg Gly Gln Thr
            20                  25                  30

Cys Tyr Arg Pro Leu Arg Gly Asp Gly Leu Ala Pro Leu Gly Arg Ser
        35                  40                  45

Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys
    50                  55                  60

Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr
65                  70                  75                  80

Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala
                85                  90                  95

Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala
            100                 105                 110

Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn
        115                 120                 125

Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala
    130                 135                 140

His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys
145                 150                 155                 160

Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe
                165                 170                 175

Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp
            180                 185                 190

Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala
        195                 200                 205

Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn
    210                 215                 220

Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn
225                 230                 235                 240

His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr
```

245 250 255

Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp
260 265 270

Leu Arg Ile Val Thr Ser Thr Tyr Lys Asp Gly Lys Gly Ala Arg Tyr
275 280 285

Asn Leu Ala Ile Glu Glu His Cys Thr Phe Gly Asp Pro Ile Val
290 295 300

<210> 6
<211> 646
<212> DNA
<213> Murinae gen. sp.

<400> 6
tcctttccta gtctgtcttc agatgaaacc tattctctgc ttgtacaaga accagtagcc 60

gtcctcaagg ccaacagcgt tggggagcgt tacgaggttt agagacgttt agccagttag 120

tttaccaaga ctctttcggg actttcacca tcaatgaatc cagtatagct gattctccaa 180

gattccctca tagaggaatt ttaattgata catctagaca cttcctgcct gtgaagacaa 240

ttttaaaaac tctggatgcc atggctttta ataagtttaa tgttcttcac tggcacatag 300

tggacgacca gtctttccct tatcagagta ccacttttcc tgagctaagc aataagggaa 360

gctactcttt gtctcatgtc tatacaccaa acgatgtccg gatggtgctg gagtacgccc 420

ggctccgagg gattcgagtc ataccagaat ttgatacccc tggccataca cagtcttggg 480

gcaaaggaca gaaaaacctt ctaactccat gttacaatca aaaaactaaa actcaagtgt 540

ttgggcctgt agacccaact gtaaacacaa cgtatgcatt ctttaacaca tttttcaaag 600

aaatcagcag tgtgtttcca gatcagttca tccacttggg aggaga 646

<210> 7
<211> 1805
<212> DNA
<213> Murinae gen. sp.

<400> 7
ggatgctttc ttcccagcga cccagactgg aaggttggtc caaagactgc ctagccagac 60

tcgcggagca gtcatgccgc agtccccgcg tagcgccccc gggctgctgc tgctgcaggc 120

gctggtgtcg ctagtgtcgc tggccctagt ggccccggcc cgactgcaac ctgcgctatg 180

gcccttcccg cgctcggtgc agatgttccc gcggctgttg tacatctccg cggaggactt 240

cagcatcgac cacagtccca attccacagc gggcccttcc tgctcgctgc tacaggaggc 300

gtttcggcga tattacaact atgtttttgg tttctacaag agacatcatg gccctgctag 360

atttcgagct gagccacagt tgcagaagct cctggtctcc attaccctcg agtcagagtg 420

cgagtccttc cctagtctgt cttcagatga aacctattct ctgcttgtac aagaaccagt 480

agccgtcctc aaggccaaca gcgtttgggg agcgttacga ggtttagaga cgtttagcca 540

gttagtttac caagactctt tcgggacttt caccatcaat gaatccagta tagctgattc 600

tccaagattc cctcatagag gaattttaat tgatacatct agacacttcc tgcctgtgaa 660

gacaatttta aaaactctgg atgccatggc ttttaataag tttaatgttc ttcactggca 720

catagtggac gaccagtctt tcccttatca gagtaccact tttcctgagc taagcaataa 780

gggaagctac tctttgtctc atgtctatac accaaacgat gtccggatgg tgctggagta 840

cgcccggctc cgagggattc gagtcatacc agaatttgat acccctggcc atacacagtc 900

ttggggcaaa ggacagaaaa accttctaac tccatgttac aatcaaaaaa ctaaaactca 960

agtgtttggg cctgtagacc caactgtaaa cacaacgtat gcattcttta acacattttt 1020

caaagaaatc agcagtgtgt ttccagatca gttcatccac ttgggaggag atgaagtaga 1080

atttcaatgt tgggcatcaa atccaaacat ccaaggtttc atgaagagaa agggctttgg 1140

cagcgatttt agaagactag aatcctttta tattaaaaag attttggaaa ttatttcatc 1200

cttaaagaag aactccattg tttggcaaga agtttttgat gataaggtgg agcttcagcc 1260

gggcacagta gtcgaagtgt ggaagagtga gcattattca tatgagctaa agcaagtcac 1320

aggctctggc ttccctgcca tcctttctgc tccttggtac ttagacctga tcagctatgg 1380

gcaagactgg aaaaactact acaaagttga gccccttaat tttgaaggct ctgagaagca 1440

gaaacaactt gttattggtg gagaagcttg cctgtgggga gaatttgtgg atgcaactaa 1500

ccttactcca agattatggc ctcgagcaag cgctgttggt gagagactct ggagccctaa 1560

aactgtcact gacctagaaa atgcctacaa acgactggcc gtgcaccgct gcagaatggt 1620

cagccgtgga atagctgcac aacctctcta tactggatac tgtaactatg agaataaaat 1680

atagaagtga cagacgtcta cagcattcca gctatgatca tgttgattct gaaatcatgt 1740

aaattaagat ttgttaggct gttttttttt taaataaacc atctttttat tgattgaatc 1800

tttct 1805

<210> 8
<211> 536
<212> PRT
<213> Murinae gen. sp.

<400> 8

Met Pro Gln Ser Pro Arg Ser Ala Pro Gly Leu Leu Leu Leu Gln Ala
1 5 10 15

Leu Val Ser Leu Val Ser Leu Ala Leu Val Ala Pro Ala Arg Leu Gln

```
            20                  25                  30

Pro Ala Leu Trp Pro Phe Pro Arg Ser Val Gln Met Phe Pro Arg Leu
        35                  40                  45

Leu Tyr Ile Ser Ala Glu Asp Phe Ser Ile Asp His Ser Pro Asn Ser
    50                  55                  60

Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr
65                  70                  75                  80

Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg
                85                  90                  95

Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu
            100                 105                 110

Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr
        115                 120                 125

Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val
    130                 135                 140

Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln
145                 150                 155                 160

Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser
                165                 170                 175

Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe
            180                 185                 190

Leu Pro Val Lys Thr Ile Leu Lys Thr Leu Asp Ala Met Ala Phe Asn
        195                 200                 205

Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro
    210                 215                 220

Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser
225                 230                 235                 240

Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr
                245                 250                 255

Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly
            260                 265                 270
```

```
His Thr Gln Ser Trp Gly Lys Gly Gln Lys Asn Leu Leu Thr Pro Cys
        275                 280                 285

Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr
    290                 295                 300

Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser
305                 310                 315                 320

Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu
                325                 330                 335

Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg
            340                 345                 350

Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys
        355                 360                 365

Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp
    370                 375                 380

Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val
385                 390                 395                 400

Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr
                405                 410                 415

Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu
            420                 425                 430

Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu
        435                 440                 445

Asn Phe Glu Gly Ser Glu Lys Gln Lys Gln Leu Val Ile Gly Gly Glu
    450                 455                 460

Ala Cys Leu Trp Gly Glu Phe Val Asp Ala Thr Asn Leu Thr Pro Arg
465                 470                 475                 480

Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg Leu Trp Ser Pro Lys
                485                 490                 495

Thr Val Thr Asp Leu Glu Asn Ala Tyr Lys Arg Leu Ala Val His Arg
            500                 505                 510

Cys Arg Met Val Ser Arg Gly Ile Ala Ala Gln Pro Leu Tyr Thr Gly
        515                 520                 525
```

Tyr Cys Asn Tyr Glu Asn Lys Ile
530 535

<210> 9
<211> 1746
<212> DNA
<213> Homo sapiens

<400> 9
ctgatccggg ccgggcggga agtcgggtcc cgaggctccg gctcggcaga ccgggcggaa 60

agcagccgag cggccatgga gctgtgcggg ctggggctgc cccggccgcc catgctgctg 120

gcgctgctgt tggcgacact gctggcggcg atgttggcgc tgctgactca ggtggcgctg 180

gtggtgcagg tggcggaggc ggctcgggcc ccgagcgtct cggccaagcc ggggccggcg 240

ctgtggcccc tgccgctctt ggtgaagatg accccgaacc tgctgcatct cgccccggag 300

aacttctaca tcagccacag ccccaattcc acggcgggcc cctcctgcac cctgctggag 360

gaagcgtttc gacgatatca tggctatatt tttggtttct acaagtggca tcatgaacct 420

gctgaattcc aggctaaaac ccaggttcag caacttcttg tctcaatcac ccttcagtca 480

gagtgtgatg ctttccccaa catatcttca gatgagtctt atactttact tgtgaaagaa 540

ccagtggctg tccttaaggc caacagagtt tggggagcat tacgaggttt agagaccttt 600

agccagttag tttatcaaga ttcttatgga actttcacca tcaatgaatc caccattatt 660

gattctccaa ggttttctca cagaggaatt ttgattgata catccagaca ttatctgcca 720

gttaagatta ttcttaaaac tctggatgcc atggctttta ataagtttaa tgttcttcac 780

tggcacatag ttgatgacca gtctttccca tatcagagca tcacttttcc tgagttaagc 840

aataaaggaa gctattcttt gtctcatgtt tatacaccaa atgatgtccg tatggtgatt 900

gaatatgcca gattacgagg aattcgagtc ctgccagaat ttgatacccc tgggcataca 960

ctatcttggg gaaaaggtca gaaagacctc ctgactccat gttacagtag acaaaacaag 1020

ttggactctt ttggacctat aaaccctact ctgaatacaa catacagctt ccttactaca 1080

tttttcaaag aaattagtga ggtgtttcca gatcaattca ttcatttggg aggagatgaa 1140

gtggaattta aatgttggga atcaaatcca aaaattcaag atttcatgag gcaaaaaggc 1200

tttggcacag attttaagaa actagaatct ttctacattc aaaaggtttt ggatattatt 1260

gcaaccataa acaagggatc cattgtctgg caggaggttt ttgatgataa agcaaagctt 1320

gcgccgggca caatagttga agtatggaaa gacagcgcat atcctgagga actcagtaga 1380

gtcacagcat ctggcttccc tgtaatcctt tctgctcctt ggtacttaga tttgattagc 1440

tatggacaag attggaggaa atactataaa gtggaacctc ttgattttgg cggtactcag 1500

aaacagaaac aacttttcat tggtggagaa gcttgtctat ggggagaata tgtggatgca 1560

actaacctca ctccaagatt atggcctcgg gcaagtgctg ttggtgagag actctggagt 1620

tccaaagatg tcagagatat ggatgacgcc tatgacagac tgacaaggca ccgctgcagg 1680

atggtcgaac gtggaatagc tgcacaacct ctttatgctg gatattgtaa ccatgagaac 1740

atgtaa 1746

<210> 10
<211> 556
<212> PRT
<213> Homo sapiens

<400> 10

Met Glu Leu Cys Gly Leu Gly Leu Pro Arg Pro Pro Met Leu Leu Ala
1 5 10 15

Leu Leu Leu Ala Thr Leu Leu Ala Ala Met Leu Ala Leu Leu Thr Gln
20 25 30

Val Ala Leu Val Val Gln Val Ala Glu Ala Ala Arg Ala Pro Ser Val
35 40 45

Ser Ala Lys Pro Gly Pro Ala Leu Trp Pro Leu Pro Leu Leu Val Lys
50 55 60

Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser
65 70 75 80

His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu
85 90 95

Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His
100 105 110

His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu
115 120 125

Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser
130 135 140

Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu
145 150 155 160

Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser
165 170 175

Gln Leu Val Tyr Gln Asp Ser Tyr Gly Thr Phe Thr Ile Asn Glu Ser
180 185 190

```
Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp
        195                 200                 205

Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp
    210                 215                 220

Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp
225                 230                 235                 240

Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn
                245                 250                 255

Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg
            260                 265                 270

Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu
        275                 280                 285

Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Lys Gly Gln Lys Asp
    290                 295                 300

Leu Leu Thr Pro Cys Tyr Ser Arg Gln Asn Lys Leu Asp Ser Phe Gly
305                 310                 315                 320

Pro Ile Asn Pro Thr Leu Asn Thr Thr Tyr Ser Phe Leu Thr Thr Phe
                325                 330                 335

Phe Lys Glu Ile Ser Glu Val Phe Pro Asp Gln Phe Ile His Leu Gly
            340                 345                 350

Gly Asp Glu Val Glu Phe Lys Cys Trp Glu Ser Asn Pro Lys Ile Gln
        355                 360                 365

Asp Phe Met Arg Gln Lys Gly Phe Gly Thr Asp Phe Lys Lys Leu Glu
    370                 375                 380

Ser Phe Tyr Ile Gln Lys Val Leu Asp Ile Ile Ala Thr Ile Asn Lys
385                 390                 395                 400

Gly Ser Ile Val Trp Gln Glu Val Phe Asp Asp Lys Ala Lys Leu Ala
                405                 410                 415

Pro Gly Thr Ile Val Glu Val Trp Lys Asp Ser Ala Tyr Pro Glu Glu
            420                 425                 430

Leu Ser Arg Val Thr Ala Ser Gly Phe Pro Val Ile Leu Ser Ala Pro
        435                 440                 445
```

```
Trp Tyr Leu Asp Leu Ile Ser Tyr Gly Gln Asp Trp Arg Lys Tyr Tyr
    450                 455                 460

Lys Val Glu Pro Leu Asp Phe Gly Gly Thr Gln Lys Gln Lys Gln Leu
465                 470                 475                 480

Phe Ile Gly Gly Glu Ala Cys Leu Trp Gly Glu Tyr Val Asp Ala Thr
                485                 490                 495

Asn Leu Thr Pro Arg Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg
            500                 505                 510

Leu Trp Ser Ser Lys Asp Val Arg Asp Met Asp Asp Ala Tyr Asp Arg
        515                 520                 525

Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln
    530                 535                 540

Pro Leu Tyr Ala Gly Tyr Cys Asn His Glu Asn Met
545                 550                 555
```

<210> 11
<211> 676
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature
<222> (604)..(604)
<223> n is a, c, g, or t

<400> 11

```
ggagctggtg ggccggagcg gcggcgccgc catgtccgac agcgagaagc tcaacctgga     60

ctccatcatc gggcgcctgc tggaagtgca gggctcacgg cctgggaaga acgtgcagct    120

gacagagaac gagatccgtg gtctgtgcct caaatcccgg gagattttcc tgagccagcc    180

cattcttctg gagcttgagg cgcccctcaa gatctgtggt gacatccatg gccagtacta    240

tgaccttcta cggctgtttg agtatggtgg cttccctcca gagagcaact acctcttctt    300

gggggattat gtagatcggg gcaagcagtc tttggagacc atctgcctgt tgctggccta    360

taagatcaga tacccggaga atttctttct acttcgtggg aaccatgagt gtgccagcat    420

caaccgcatt tatggcttct atgatgaatg caagagaaga tacaacatca aactgtggaa    480

gacgttcact gactgcttca actgcctgcc cattgcagcc attgtggatg agaagatctt    540

ctgctgccac gggggcctgt ctccagactt gcaatccatg gagcagatta ggcgtattat    600

gcgngccaca gacgtgcctg accagggcct actgtgtgat ctcctgtggt ctgaccctga    660
```

caagaaatag cctcca 676

<210> 12
<211> 1369
<212> DNA
<213> Murinae gen. sp.

<400> 12
ggaggcagga gagggcccgg agctggtggg ccggagcggc ggcgccgcca tgtccgacag 60

cgagaagctc aacctggact ccatcatcgg gcgcctgctg gaagtgcagg gctcacggcc 120

tgggaagaac gtgcagctga cagagaacga gatccgtggt ctgtgcctca aatcccggga 180

gattttcctg agccagccca ttcttctgga gcttgaggcg cccctcaaga tctgtggtga 240

catccatggc cagtactatg accttctacg gctgtttgag tatggtggct tccctccaga 300

gagcaactac ctcttcttgg gggattatgt agatcggggc aagcagtctt tggagaccat 360

ctgcctgttg ctggcctata agatcagata cccggagaat ttctttctac ttcgtgggaa 420

ccatgagtgt gccagcatca accgcattta tggcttctat gatgaatgca agagaagata 480

caacatcaaa ctgtggaaga cgttcactga ctgcttcaac tgcctgccca ttgcagccat 540

tgtggatgag aagatcttct gctgccacgg gggcctgtct ccagacttgc aatccatgga 600

gcagattagg cgtattatgc ggcccacaga cgtgcctgac cagggcctac tgtgtgatct 660

cctgtggtct gaccctgaca aggatgttca aggctggggc gagaatgacc gtggtgtctc 720

ctttaccttt ggggctgagg tggtagccaa gttcctgcac aagcatgatt tggacctcat 780

ctgcagagca catcaggttg tagaagatgg ctatgagttc tttgccaaga gacagttggt 840

gacactcttc tcagctccca actactgtgg agagtttgac aatgctggtg ccatgatgag 900

tgtggatgag accctcatgt gttccttcca gatcctcaag cccgctgata agaataaggg 960

caagtatggg cagttcagcg gcctgaaccc cggaggccgg cccatcactc caccccgcaa 1020

ttctgccaaa gccaagaaat agcctccatg tgctgccctt ctgccccaga tcgtttgtac 1080

agaaatcatg ctgccatggg tcacactggc ctctcaggcc cacccgtcac ggggaacaca 1140

cagcgttaag tgtctttcct ttatttttta aagaatcaat agcagcatct aatctcccag 1200

ggctccctcc caccagcacc tgtggtggct gcaagtggaa tcctggggcc aaggctgcag 1260

ctcagggcaa tggcagacca gattgtgggt ctccagcctt gcatggctgg cagccagatc 1320

ctggggcaac ccatctggtc tcttgaataa aggtcaaagc tggattctc 1369

<210> 13
<211> 330
<212> PRT
<213> Murinae gen. sp.

<400> 13

```
Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
1               5                  10                  15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
            20                  25                  30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
        35                  40                  45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
    50                  55                  60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65                  70                  75                  80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
                85                  90                  95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
            100                 105                 110

Arg Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
        115                 120                 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
    130                 135                 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145                 150                 155                 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165                 170                 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180                 185                 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195                 200                 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210                 215                 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225                 230                 235                 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245                 250                 255
```

```
Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260                 265                 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275                 280                 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
    290                 295                 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305                 310                 315                 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
                325                 330
```

<210> 14
<211> 993
<212> DNA
<213> Homo sapiens

<400> 14

```
atgtccgaca gcgagaagct caacctggac tcgatcatcg ggcgcctgct ggaagtgcag     60

ggctcgcggc ctggcaagaa tgtacagctg acagagaacg agatccgcgg tctgtgcctg    120

aaatcccggg agatttttct gagccagccc attcttctgg agctggaggc acccctcaag    180

atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggt    240

ttccctcccg agagcaacta cctctttctg ggggactatg tggacagggg caagcagtcc    300

ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg    360

ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc    420

aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc    480

atcgcggcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg    540

cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg    600

ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac    660

cgtggcgtct cttttacctt tggagccgag gtggtggcca agttcctcca caagcacgac    720

ttggacctca tctgccgagc acaccaggtg gtagaagacg gctacgagtt ctttgccaag    780

cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagtttga caatgctggc    840

gccatgatga gtgtggacga gaccctcatg tgctctttcc agatcctcaa gcccgccgac    900

aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc    960

ccaccccgca attccgccaa agccaagaaa tag                                 993
```

<210> 15
<211> 330
<212> PRT
<213> Homo sapiens

<400> 15

```
Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
1               5                  10                  15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
            20                  25                  30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
        35                  40                  45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
    50                  55                  60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65                  70                  75                  80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
                85                  90                  95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
            100                 105                 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
        115                 120                 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
    130                 135                 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145                 150                 155                 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165                 170                 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180                 185                 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195                 200                 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210                 215                 220
```

```
Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225                 230                 235                 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245                 250                 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260                 265                 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275                 280                 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
    290                 295                 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305                 310                 315                 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
                325                 330
```

<210> 16
<211> 702
<212> DNA
<213> Murinae gen. sp.

<400> 16

```
ggcatgacag gcagtgagca ggtgatgagc caggttgtgg atctctttag tgagggaata     60

ggctgctgga gatatggctg tggtctacaa ggaggctggg gaactagcaa ggagatgctc    120

tctcagctat cacagcctta cagcaaagcc actatctctt tggattttga aattttctct    180

gccatgccta tgactatttt aaaattgggc aaagtatatc catttcagag gggctttttc    240

tgtactgaca acagcgtgaa gtacccgtac catgacagta ccatcccgtc ccgtatactc    300

gccatactgg ggcttggctt acccattttc tctatgagta tggagaatct ctgtctgttt    360

actttaatgt cttgcattcg aattcctttg tcggcaatcc ctacatagcc accatttaca    420

aagccgtcgg agccttttgt tcggagtctc agctagtcag tccttgactg acatcgctaa    480

gtatactata ggcagtttgc ggccgcactt cttggctatc tgtaacccag actggtcaaa    540

aatcaactgc agtgatggct atattgagga ctacatatgt caagggaatg aagagaaagt    600

caaggagggc aggttgtctt tctactcggg acactcttca ttctctatgt actgcatgct    660

gtttgtcgca ctttatcttc aagccaggat gaagggagac tg                       702
```

<210> 17
<211> 1432
<212> DNA
<213> Murinae gen. sp.

<400> 17
catccttaga gctcgcccgg cctgttggag agggcacagg gcagcggagg gcgattggcc 60

gcgacgagcc agcactgaga gagcaggcgc ctgaggcgac agatcggcgg ccactcggtg 120

gcagggcggc ccaatccaaa ctgccctggt ccctgctccc gtcagtctaa gaggctcgca 180

gtcgcttggg gcggccgcca tcccgagggc ggggctctgg gaattgggta tctggaccgc 240

cgcggtctgt tcctcccgcc actcgcacca ggtggtgaca ccatccagcc ggtgaccatg 300

ttcgacaaga cgcggctgcc gtacgtggcc ctcgatgtga tttgcgtgtt gctggctgga 360

ttgccttttg caattcttac ttcaaggcat acccccttcc agcgaggaat attctgtaat 420

gatgactcca tcaagtaccc ttacaaggaa gacaccatac cttatgcctt attaggtgga 480

atagtcattc cattctgtat tatcgttatg agtattggag aatctctgtc tgtttacttt 540

aatgtcttgc attcgaattc ctttgtcggc aatccctaca tagccaccat ttacaaagcc 600

gtcggagcct ttttgttcgg agtctcagct agtcagtcct tgactgacat cgctaagtat 660

actataggca gtttgcggcc gcacttcttg gctatctgta acccagactg gtcaaaaatc 720

aactgcagtg atggctatat tgaggactac atatgtcaag ggaatgaaga gaaagtcaag 780

gagggcaggt tgtctttcta ctcgggacac tcttcattct ctatgtactg catgctgttt 840

gtcgcacttt atcttcaagc caggatgaag ggagactggg caagactctt acgacccatg 900

ctccagtttg ggctcattgc tttttccata tatgtgggcc tttctcgagt gtctgactac 960

aaacaccact ggagtgacgt cacagttgga ctcattcagg gagctgctat ggctatactg 1020

gttgctttgt atgtatccga tttcttcaag gacacacatt cttacaaaga gagaaaggaa 1080

gaggatccac acacgactct ccatgaaacc gccagttcac ggaactactg ggcgctggcc 1140

cgcttcaaag gcaacagctg gaggctaaag gcaggggat gcgtattact tcctgctgta 1200

cagaccattc tataaaggac tgctgctatc tatacctcct ggatgcccat tttatgtgtg 1260

tacagttact tctaacacaa tgagtaacag ttcaattaaa gaaaatgaag cctgtcacta 1320

aaacactgtc ccacctgtac atttttattg aaagacgcta tgtacaaatg tgtatgttac 1380

atgccttctc agaatgatgt tgacttaaat ataataaaaa gcttgtgaac ca 1432

<210> 18
<211> 378
<212> PRT
<213> Murinae gen. sp.

<400> 18

Glu Ser Arg Arg Leu Arg Arg Gln Ile Gly Gly His Ser Val Ala Gly
1 5 10 15

Arg Pro Asn Pro Asn Cys Pro Gly Pro Cys Ser Arg Gln Ser Lys Arg

```
            20                  25                  30

Leu Ala Val Ala Trp Gly Gly Arg His Pro Glu Gly Gly Ala Leu Gly
        35                  40                  45

Ile Gly Tyr Leu Asp Arg Arg Gly Leu Phe Leu Pro Pro Leu Ala Pro
    50                  55                  60

Gly Gly Asp Thr Ile Gln Pro Val Thr Met Phe Asp Lys Thr Arg Leu
65                  70                  75                  80

Pro Tyr Val Ala Leu Asp Val Ile Cys Val Leu Leu Ala Gly Leu Pro
                85                  90                  95

Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg Gly Ile Phe
            100                 105                 110

Cys Asn Asp Asp Ser Ile Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro
        115                 120                 125

Tyr Ala Leu Leu Gly Gly Ile Val Ile Pro Phe Cys Ile Ile Val Met
    130                 135                 140

Ser Ile Gly Glu Ser Leu Ser Val Tyr Phe Asn Val Leu His Ser Asn
145                 150                 155                 160

Ser Phe Val Gly Asn Pro Tyr Ile Ala Thr Ile Tyr Lys Ala Val Gly
                165                 170                 175

Ala Phe Leu Phe Gly Val Ser Ala Ser Gln Ser Leu Thr Asp Ile Ala
            180                 185                 190

Lys Tyr Thr Ile Gly Ser Leu Arg Pro His Phe Leu Ala Ile Cys Asn
        195                 200                 205

Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Asp Tyr
    210                 215                 220

Ile Cys Gln Gly Asn Glu Glu Lys Val Lys Glu Gly Arg Leu Ser Phe
225                 230                 235                 240

Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala
                245                 250                 255

Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg
            260                 265                 270
```

```
Pro Met Leu Gln Phe Gly Leu Ile Ala Phe Ser Ile Tyr Val Gly Leu
        275                 280                 285

Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Thr Val Gly
    290                 295                 300

Leu Ile Gln Gly Ala Ala Met Ala Ile Leu Val Ala Leu Tyr Val Ser
305                 310                 315                 320

Asp Phe Phe Lys Asp Thr His Ser Tyr Lys Glu Arg Lys Glu Glu Asp
                325                 330                 335

Pro His Thr Thr Leu His Glu Thr Ala Ser Ser Arg Asn Tyr Trp Ala
            340                 345                 350

Leu Ala Arg Phe Lys Gly Asn Ser Trp Arg Leu Lys Ala Gly Gly Cys
        355                 360                 365

Val Leu Leu Pro Ala Val Gln Thr Ile Leu
    370                 375
```

<210> 19
<211> 1626
<212> DNA
<213> Homo sapiens

<400> 19

```
tcagcgggag gggctggacc ccgcgttcct cctccctgcc ggtccccatc cttaaagcga     60

gagtctggac gccccgcctg tgggagagag cgccgggatc cggacgggga gcaaccgggg    120

caggccgtgc cggctgagga ggtcctgagg ctacagagct gccgcggctg gcacacgagc    180

gcctcggcac taaccgagtg ttcgcggggg ctgtgagggg agggccccgg gcgccattgc    240

tggcggtggg agcgccgccc ggtctcagcc cgccctcggc tgctctcctc ctccggctgg    300

gaggggccgt agctcggggc cgtcgccagc cccggcccgg gctcgagaat caagggcctc    360

ggccgccgtc ccgcagctca gtccatcgcc cttgccgggc agcccgggca gagaccatgt    420

ttgacaagac gcggctgccg tacgtggccc tcgatgtgct ctgcgtgttg ctggcttcca    480

tgcctatggc tgttctaaaa ttgggccaaa tatatccatt tcagagaggc tttttctgta    540

aagacaacag catcaactat ccgtaccatg acagtaccgt cacatccact gtcctcatcc    600

tagtgggggt tggcttgccc atttcctcta ttattcttgg agaaaccctg tctgtttact    660

gtaacctttt gcactcaaat tcctttatca ggaataacta catagccact atttacaaag    720

ccattggaac ctttttattt ggtgcagctg ctagtcagtc cctgactgac attgccaagt    780

attcaatagg cagactgcgg cctcacttct tggatgtttg tgatccagat tggtcaaaaa    840

tcaactgcag cgatggttac attgaatact acatatgtcg agggaatgca gaaagagtta    900
```

aggaaggcag gttgtccttc tattcaggcc actcttcgtt ttccatgtac tgcatgctgt 960

ttgtggcact ttatcttcaa gccaggatga agggagactg ggcaagactc ttacgcccca 1020

cactgcaatt tggtcttgtt gccgtatcca tttatgtggg cctttctcga gtttctgatt 1080

ataaacacca ctggagcgat gtgttgactg gactcattca gggagctctg gttgcaatat 1140

tagttgctgt atatgtatcg gatttcttca aagaaagaac ttcttttaaa gaaagaaaag 1200

aggaggactc tcatacaact ctgcatgaaa caccaacaac tgggaatcac tatccgagca 1260

atcaccagcc ttgaaaggca gcagggtgcc caggtgaagc tggcctgttt tctaaaggaa 1320

aatgattgcc acaaggcaag aggatgcatc tttcttcctg gtgtacaagc ctttaaagac 1380

ttctgctgct gctatgcctc ttggatgcac actttgtgtg tacatagtta cctttaactc 1440

agtggttatc taatagctct aaactcatta aaaaaactcc aagccttcca ccaaaacagt 1500

gccccacctg tatacatttt tattaaaaaa atgtaatgct tatgtataaa catgtatgta 1560

atatgctttc tatgaatgat gtttgattta aatataatac atattaaaat gtatgggaga 1620

accaaa 1626

<210> 20
<211> 378
<212> PRT
<213> Homo sapiens

<400> 20

Gly Gly Pro Glu Ala Thr Glu Leu Pro Arg Leu Ala His Glu Arg Leu
1 5 10 15

Gly Thr Asn Arg Val Phe Ala Gly Ala Val Arg Gly Gly Pro Arg Ala
20 25 30

Pro Leu Leu Ala Val Gly Ala Pro Pro Gly Leu Ser Pro Pro Ser Ala
35 40 45

Ala Leu Leu Leu Arg Leu Gly Gly Ala Val Ala Arg Gly Arg Arg Gln
50 55 60

Pro Arg Pro Gly Leu Glu Asn Gln Gly Pro Arg Pro Pro Ser Arg Ser
65 70 75 80

Ser Val His Arg Pro Cys Arg Ala Ala Arg Ala Glu Thr Met Phe Asp
85 90 95

Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu
100 105 110

```
Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe
        115                 120                 125

Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His
    130                 135                 140

Asp Ser Thr Val Thr Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu
145                 150                 155                 160

Pro Ile Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn
                165                 170                 175

Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile
            180                 185                 190

Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser
        195                 200                 205

Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe
    210                 215                 220

Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly
225                 230                 235                 240

Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu
                245                 250                 255

Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys
            260                 265                 270

Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp
        275                 280                 285

Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser
    290                 295                 300

Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser
305                 310                 315                 320

Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val
                325                 330                 335

Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu
            340                 345                 350

Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr
        355                 360                 365
```

Gly Asn His Tyr Pro Ser Asn His Gln Pro
370 375

<210> 21
<211> 816
<212> DNA
<213> Homo sapiens

<400> 21
atttattccc ttttgctagc tggattgcct tttgcaattc ttacttcaag gcataccccc 60

ttccaacgag gagtattctg taatgatgag tccatcaagt acccttacaa agaagacacc 120

ataccttatg cgttattagg tggaataatc attccattca gtattatcgt tattattctt 180

ggagaaaccc tgtctgttta ctgtaacctt ttgcactcaa attcctttat caggaataac 240

tacatagcca ctatttacaa agccattgga acctttttat ttggtgcagc tgctagtcag 300

tccctgactg acattgccaa gtattcaata ggcagactgc ggcctcactt cttggatgtt 360

tgtgatccag attggtcaaa aatcaactgc agcgatggtt acattgaata ctacatatgt 420

cgagggaatg cagaaagagt taaggaaggc aggttgtcct tctattcagg ccactcttcg 480

ttttccatgt actgcatgct gtttgtggca ctttatcttc aagccaggat gaagggagac 540

tgggcaagac tcttacgccc cacactgcaa tttggtcttg ttgccgtatc catttatgtg 600

ggcctttctc gagtttctga ttataaacac cactggagcg atgtgttgac tggactcatt 660

cagggagctc tggttgcaat attagttgct gtatatgtat cggatttctt caaagaaaga 720

acttctttta aagaaagaaa agaggaggac tctcatacaa ctctgcatga aacaccaaca 780

actgggaatc actatccgag caatcaccag ccttga 816

<210> 22
<211> 271
<212> PRT
<213> Homo sapiens

<400> 22

Ile Tyr Ser Leu Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser
1 5 10 15

Arg His Thr Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile
20 25 30

Lys Tyr Pro Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly
35 40 45

Ile Ile Ile Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu
50 55 60

```
Ser Val Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn
65                  70                  75                  80

Tyr Ile Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala
                85                  90                  95

Ala Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg
            100                 105                 110

Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile
        115                 120                 125

Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala
    130                 135                 140

Glu Arg Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser
145                 150                 155                 160

Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg
                165                 170                 175

Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly
            180                 185                 190

Leu Val Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr
        195                 200                 205

Lys His His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu
    210                 215                 220

Val Ala Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg
225                 230                 235                 240

Thr Ser Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His
                245                 250                 255

Glu Thr Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
            260                 265                 270


<210>  23
<211>  840
<212>  DNA
<213>  Murinae gen. sp.


<220>
<221>  misc_feature
<222>  (474)..(474)
<223>  n is a, c, g, or t
```

<400> 23
ccgaagtaag tttgccagtt ttctgtctta tactgaggtt cgccgggtca tggtgccagc 60

ctgactgaga agaggacgct cccgggaaac gaatgaggaa ccacctcctc ctgctgttca 120

agtacagggg cctggtgcgc aaagggaaga aaagcaaaag acgaaaatgg ctaaatttaa 180

gatccgtcca gccactgcct ctgactgcag tgacatcctg cgactgatca aggaactggc 240

taaatatgaa tacatggaag atcaagtcat tttaactgag aaagatctcc aagaggatgg 300

ctttggagaa caccccttct accactgcct ggttgcagaa gtgcctaaag agcactggac 360

ccctgaagga catagcattg ttgggttcgc catgtactat tttacctatg acccatggat 420

tggcaagttg ctgtatcttg aagacttctt cgtgatgagt gattacagag gctntggtat 480

aggatcagaa attttgaaga atctaagcca ggttgccatg aagtgtcgct gcagcagtat 540

gcacttcttg gtagcagaat ggaatgaacc atctatcaac ttctacaaaa gaagaggtgc 600

ttcggatctg tccagtgaag agggatggga ggctcttcaa gattgacaag agtacttgct 660

aaaaatggca gcagaggagt gaggcgtgcc ggtgtagaac atgacaacct ccattgtgct 720

ttagaataat tctcagcttc ccttgctttc tatcttgtgg tgtaggtgaa ataatagagc 780

gagccaccat tccaaagctt tattaccagt gacgtgttgc atgtttgaaa tcggtctggt 840

<210> 24
<211> 1052
<212> DNA
<213> Murinae gen. sp.

<400> 24
gctgcgcagt ttccccgaag taagtttgcc agttttctgt cttatactga ggttcgccgg 60

gtcatggtgc cagcctgact gagaagagga cgctcccggg aaacgaatga ggaaccacct 120

cctcctgctg ttcaagtaca ggggcctggt gcgcaaaggg aagaaaagca aaagacgaaa 180

atggctaaat ttaagatccg tccagccact gcctctgact gcagtgacat cctgcgactg 240

atcaaggaac tggctaaata tgaatacatg gaagatcaag tcattttaac tgagaaagat 300

ctccaagagg atggctttgg agaacacccc ttctaccact gcctggttgc agaagtgcct 360

aaagagcact ggacccctga aggacatagc attgttgggt tcgccatgta ctattttacc 420

tatgacccat ggattggcaa gttgctgtat cttgaagact tcttcgtgat gagtgattac 480

agaggctttg gtataggatc agaaattttg aagaatctaa gccaggttgc catgaagtgt 540

cgctgcagca gtatgcactt cttggtagca gaatggaatg aaccatctat caacttctac 600

aaaagaagag gtgcttcgga tctgtccagt gaagagggat ggaggctctt caagattgac 660

aaagagtact tgctaaaaat ggcagcagag gagtgaggcg tgccggtgta gacaatgaca 720

acctccattg tgctttagaa taattctcag cttcccttgc tttctatctt gtgtgtagtg 780

aaataataga gcgagcaccc attccaaagc tttattacca gtgacgttgt tgcatgtttg 840

aaattcggtc tgtttaaagt ggcagtcatg tatgtggttt ggaggcagaa ttcttgaaca 900

tcttttgatg aagaacaagg tggtatgatc ttactatata agaaaaacaa aacttcattc 960

ttgtgagtca tttaaatgtg tacaatgtac acactggtac ttagagtttc tgttttgatt 1020

ctttttttt taaataaact actctttgat tt 1052

<210> 25
<211> 171
<212> PRT
<213> Murinae gen. sp.

<400> 25

Met Ala Lys Phe Lys Ile Arg Pro Ala Thr Ala Ser Asp Cys Ser Asp
1 5 10 15

Ile Leu Arg Leu Ile Lys Glu Leu Ala Lys Tyr Glu Tyr Met Glu Asp
20 25 30

Gln Val Ile Leu Thr Glu Lys Asp Leu Gln Glu Asp Gly Phe Gly Glu
35 40 45

His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu His Trp
50 55 60

Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr Tyr Phe Thr
65 70 75 80

Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe Val
85 90 95

Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly Ser Glu Ile Leu Lys Asn
100 105 110

Leu Ser Gln Val Ala Met Lys Cys Arg Cys Ser Ser Met His Phe Leu
115 120 125

Val Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly
130 135 140

Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg Leu Phe Lys Ile Asp
145 150 155 160

Lys Glu Tyr Leu Leu Lys Met Ala Ala Glu Glu
165 170

<210> 26
<211> 1111

<212> DNA
<213> Homo sapiens

<400> 26
gcgcagctct tagtcgcggg ccgactggtg tttatccgtc actcgccgag gttccttggg 60

tcatggtgcc agcctgactg agaagaggac gctcccggga gacgaatgag gaaccacctc 120

ctcctactgt tcaagtacag gggcctggtc cgcaaaggga agaaaagcaa aagacgaaaa 180

tggctaaatt cgtgatccgc ccagccactg ccgccgactg cagtgacata ctgcggctga 240

tcaaggagct ggctaaatat gaatacatgg aagaacaagt aatcttaact gaaaaagatc 300

tgctagaaga tggttttgga gagcacccct tttaccactg cctggttgca gaagtgccga 360

aagagcactg gactccggaa ggtaacccct cgccctttcc agaagccaga gagaccaaca 420

ttgttggttt tgccatgtac tattttacct atgacccgtg gattggcaag ttattgtatc 480

ttgaggactt cttcgtgatg agtgattata gaggtacgat tgagctttgg cataggatca 540

gaaattctga agaatctaag ccaggttgca atgaggtgtc gctggcagca tgcacttctt 600

gggcagaatg gaatgaacca tccatcaact tctataaaag aagaggtgct tctgatctgt 660

ccagtgaaga gggttggaga ctgttcaaga tcgacaagga gtacttgcta aaaatggcaa 720

cagaggagtg aggagtgctg ctgtagatga caacctccat tctattttag aataaattcc 780

caacttctct tgctttctat gctgtttgta gtgaaataat agaatgagca cccattccaa 840

agctttatta ccagtggcgt tgttgcatgt ttgaaatgag gtctgtttaa agtggcaatc 900

tcagatgcag tttggagagt cagatctttc tccttgaata tctttcgata aacaacaagg 960

tggtgtgatc ttaatatatt tgaaaaaaac ttcattctcg tgagtcattt aaatgtgtac 1020

aatgtacaca ctggtactta gagtttctgt ttgattcttt tttaataaac tactctttga 1080

tttaattcta aaaaaaaaaa aaaaaaagac a 1111

<210> 27
<211> 190
<212> PRT
<213> Homo sapiens

<400> 27

Glu Pro Pro Pro Pro Thr Val Gln Val Gln Gly Pro Gly Pro Gln Arg
1 5 10 15

Glu Glu Lys Gln Lys Thr Lys Met Ala Lys Phe Val Ile Arg Pro Ala
20 25 30

Thr Ala Ala Asp Cys Ser Asp Ile Leu Arg Leu Ile Lys Glu Leu Ala
35 40 45

Lys Tyr Glu Tyr Met Glu Glu Gln Val Ile Leu Thr Glu Lys Asp Leu

50 55 60

Leu Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Val Ala
65 70 75 80

Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly Asn Pro Ser Pro Phe
85 90 95

Pro Glu Ala Arg Glu Thr Asn Ile Val Gly Phe Ala Met Tyr Tyr Phe
100 105 110

Thr Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe
115 120 125

Val Met Ser Asp Tyr Arg Gly Thr Ile Glu Leu Trp His Arg Ile Arg
130 135 140

Asn Ser Glu Glu Ser Lys Pro Gly Cys Asn Glu Val Ser Leu Ala Ala
145 150 155 160

Cys Thr Ser Trp Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys
165 170 175

Arg Arg Gly Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg
180 185 190

<210> 28
<211> 745
<212> DNA
<213> Murinae gen. sp.

<400> 28
aatctatgga gcagattcgg cgaattatga gaccaactga tgtaccagat caaggtcttc 60

tttgtgatct ttggtggtct gaccccgatg aaagatgtct taggctgggg tgaaaatgac 120

agaggagtgt ccttcacatt tggtgcagaa gtggttgcaa aatttctcca taagcatgat 180

tcggatctta tatgtagagc ccatcaggtg gttgaagatg gctatgagtt tttcgcaaag 240

aggcagttag tcactctgtt gttctgcgag cccaactact gtggcgagtt tgacaatgca 300

ggcgccatga tgagtgtgga tgagaccctc atgtgttcct tccagatttt aaagcctgca 360

gagaaaaaga agcccaacgc cacgagacct gtcacaccac cacggggtat gatcacaaag 420

caagcaaaga aatagatgtc acttgacact gcctggttgg gacttgtaac atagcgttca 480

taaccttcct ttttaaactg tgatgtgctg gtcagcttgc ccaggtagac ctgtctgtcg 540

ggccctcctc catttgatta ctgctggcac ttgctggtta tagcagcaag ccaagcactt 600

cattctcaag agagcatttg gttctgaacc tctgttccct ttgtggacag ctctgatgat 660

ggtgttaagc tgtacaccct ggcaggttat cctgtctgag gagaaagtgt acaattgatc 720

ttttttagt ttagtataag tcatg 745

<210> 29
<211> 2127
<212> DNA
<213> Murinae gen. sp.

<400> 29
gctgctgcgg gagggtcggc ggcgggacgg cgatggcgga tatcgacaaa ctcaacatcg 60

acagcatcat ccaacggctg ctggaagtga gagggtccaa gccaggcaag aatgtccagc 120

tccaggagaa cgagatccga ggactctgcc tgaagtctcg ggagatcttc ctcagtcagc 180

ctatcctttt agaacttgaa gcaccactca agatatgtgg tgacatccac gggcagtact 240

atgatttgct ccgtctgttt gaatacggtg gctttcctcc agagagcaac tatttgtttc 300

tcggggacta tgtggacagg ggcaagcagt ccctggagac aatctgcctc ttgctggcct 360

acaaaatcaa gtatccggag aacttctttc ttctcagagg gaaccacgag tgcgccagca 420

tcaataggat ctacggattt tatgatgagt gtaaaagaag atacaacatt aagctgtgga 480

aaacgttcac agactgtttt aactgcttgc cgatagcagc catcgtggac gagaagatat 540

tctgctgtca tggaggttta tcaccagatc ttcaatctat ggagcagatt cggcgaatta 600

tgagaccaac tgatgtacca gatcaaggtc ttctttgtga tcttttgtgg tctgaccccg 660

ataaagatgt cttaggctgg ggtgaaaatg acagaggagt gtccttcaca tttggtgcag 720

aagtggttgc aaaatttctc cataagcatg atttggatct tatatgtaga gcccatcagg 780

tggttgaaga tggctatgag ttttttgcaa agaggcagtt agtcactctg ttttctgcac 840

ccaactactg tggcgagttt gacaatgcag gcgccatgat gagtgtggat gagaccctca 900

tgtgttcctt ccagatttta aagcctgcag agaaaaagaa gcccaacgcc acgagacctg 960

tcacaccacc acggggtatg atcacaaagc aagcaaagaa atagatgtca cttgacactg 1020

cctggttggg acttgtaaca tagcgttcat aaccttcctt tttaaactgt gatgtgctgg 1080

tcagcttgcc caggtagacc tgtctgtcgg gccctcctcc atttgattac tgctggcact 1140

tgctggttat agcagcaagc caagcacttc attctcaaga gagcattttg ttttgaacct 1200

ctgttccctt tgtggacagc tctgatgatg gtgttaagct gtacaccctg gcaggttatc 1260

ctgtctgagg agaaagtgta caattgatct ttttttaatt tagtataagt catgaataat 1320

gtaaatgcct gttttcttta ggatataaag agagccttag agtgcgtgag tctctacatg 1380

taattgtcat aaatgcattc tgttgataca aaccactgtg aacaattttt tttccagttt 1440

gtttgaaagg gactgctttc cctcattgtc ttgtcatgta caaactagtg tctgcagctg 1500

tggcagcagg agtgacctgc ctgccgccag ccctgcccag actatctgaa gcacactcct 1560

tcccactgca catttaataa tgattaaagc cattcttttc aatgtctgtg attccttcct 1620

aaagccaaag tttctgttgg actgtatggc acgccctggg gatgaggtgg ccagggcatc 1680

gaggctgcgt gcacaggccg cctccctccg tggggcctca gaagcaggtt attttaacta 1740

gcaatagtgg tatagtgctg agtaagctat taatgatgga agttaatgac actttgtaca 1800

gttcccatat agtctattca ctgagtgatc tttttacagt tggatcaggc ctgaacccgt 1860

ccattcagaa agcttcaaat tatagaaaca acactgtcct atacgagtga ccgataatgc 1920

tttctttggc tacattcttt attctgcggt gacattgagg cttataaatc aaaaggaact 1980

aacttgccgt ccaccggttt atacagaact cacagtatct atgacttttt taaactacga 2040

cctgttaaat gaatctgttt gcacagatgc ccgtgtacaa tgccatgtgc tgagaatggt 2100

ttcagactta ttaaatgcaa gcttgtt 2127

<210> 30
<211> 323
<212> PRT
<213> Murinae gen. sp.

<400> 30

Met Ala Asp Ile Asp Lys Leu Asn Ile Asp Ser Ile Ile Gln Arg Leu
1 5 10 15

Leu Glu Val Arg Gly Ser Lys Pro Gly Lys Asn Val Gln Leu Gln Glu
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala
115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
130 135 140

```
Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145                 150                 155                 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
                165                 170                 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
            180                 185                 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
        195                 200                 205

Pro Asp Lys Asp Val Leu Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
    210                 215                 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225                 230                 235                 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
                245                 250                 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
            260                 265                 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
        275                 280                 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Glu Lys Lys Lys Pro
    290                 295                 300

Asn Ala Thr Arg Pro Val Thr Pro Pro Arg Gly Met Ile Thr Lys Gln
305                 310                 315                 320

Ala Lys Lys
```

<210> 31
<211> 993
<212> DNA
<213> Homo sapiens

<400> 31
atgtccgaca gcgagaagct caacctggac tcgatcatcg ggcgcctgct ggaagtgcag 60

ggctcgcggc ctggcaagaa tgtacagctg acagagaacg agatccgcgg tctgtgcctg 120

aaatcccggg agatttttct gagccagccc attcttctgg agctggaggc acccctcaag 180

atctgcggtg acatacacgg ccagtactac gaccttctgc gactatttga gtatggcggt 240

ttccctcccg agagcaacta cctctttctg ggggactatg tggacagggg caagcagtcc 300

ttggagacca tctgcctgct gctggcctat aagatcaagt accccgagaa cttcttcctg 360

ctccgtggga accacgagtg tgccagcatc aaccgcatct atggtttcta cgatgagtgc 420

aagagacgct acaacatcaa actgtggaaa accttcactg actgcttcaa ctgcctgccc 480

atcgcggcca tagtggacga aaagatcttc tgctgccacg gaggcctgtc cccggacctg 540

cagtctatgg agcagattcg gcggatcatg cggcccacag atgtgcctga ccagggcctg 600

ctgtgtgacc tgctgtggtc tgaccctgac aaggacgtgc agggctgggg cgagaacgac 660

cgtggcgtct cttttacctt tggagccgag gtggtggcca agttcctcca caagcacgac 720

ttggacctca tctgccgagc acaccaggtg gtagaagacg gctacgagtt ctttgccaag 780

cggcagctgg tgacactttt ctcagctccc aactactgtg gcgagtttga caatgctggc 840

gccatgatga gtgtggacga gaccctcatg tgctctttcc agatcctcaa gcccgccgac 900

aagaacaagg ggaagtacgg gcagttcagt ggcctgaacc ctggaggccg acccatcacc 960

ccaccccgca attccgccaa agccaagaaa tag 993

<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

<400> 32

Met Ser Asp Ser Glu Lys Leu Asn Leu Asp Ser Ile Ile Gly Arg Leu
1 5 10 15

Leu Glu Val Gln Gly Ser Arg Pro Gly Lys Asn Val Gln Leu Thr Glu
20 25 30

Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile Phe Leu Ser
35 40 45

Gln Pro Ile Leu Leu Glu Leu Glu Ala Pro Leu Lys Ile Cys Gly Asp
50 55 60

Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu Tyr Gly Gly
65 70 75 80

Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg
85 90 95

Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala Tyr Lys Ile
100 105 110

Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His Glu Cys Ala

115 120 125

Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys Arg Arg Tyr
130 135 140

Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn Cys Leu Pro
145 150 155 160

Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His Gly Gly Leu
165 170 175

Ser Pro Asp Leu Gln Ser Met Glu Gln Ile Arg Arg Ile Met Arg Pro
180 185 190

Thr Asp Val Pro Asp Gln Gly Leu Leu Cys Asp Leu Leu Trp Ser Asp
195 200 205

Pro Asp Lys Asp Val Gln Gly Trp Gly Glu Asn Asp Arg Gly Val Ser
210 215 220

Phe Thr Phe Gly Ala Glu Val Val Ala Lys Phe Leu His Lys His Asp
225 230 235 240

Leu Asp Leu Ile Cys Arg Ala His Gln Val Val Glu Asp Gly Tyr Glu
245 250 255

Phe Phe Ala Lys Arg Gln Leu Val Thr Leu Phe Ser Ala Pro Asn Tyr
260 265 270

Cys Gly Glu Phe Asp Asn Ala Gly Ala Met Met Ser Val Asp Glu Thr
275 280 285

Leu Met Cys Ser Phe Gln Ile Leu Lys Pro Ala Asp Lys Asn Lys Gly
290 295 300

Lys Tyr Gly Gln Phe Ser Gly Leu Asn Pro Gly Gly Arg Pro Ile Thr
305 310 315 320

Pro Pro Arg Asn Ser Ala Lys Ala Lys Lys
325 330

<210> 33
<211> 747
<212> DNA
<213> Murinae gen. sp.

<220>
<221> misc_feature

<222> (298)..(298)
<223> n is a, c, g, or t

<400> 33
cgacaagtca tgctgctcgc tatgaataag gttgaaggag acaacattag cggcgtttgc 60

ttcgttggcc tgtatgacct ggacgcctct cgctacttcg tccttctgcc tctgtgcctc 120

tgcgtatttg ttgagctggg agagtagccc agtggtacag cgcccacctg gaatacttga 180

ggacctgggg ttgtctccca gcactgcaaa aggaaaattc actgttacag tcttccttgc 240

acttaaacca gctttgtcta ttgtttttt ggtttggctt tgttactttt gttgctgntt 300

atttttgttg ttgttgtttg tttgtttgag acagggtttt tttgctagcc ctgactgtcc 360

tgaaactccc tctgtagacc aggctggcct caaacttaca gagatccgcc tgcctcagcc 420

tcccaagtgc tgggaataat ggtgtggtca ccaccgccca gccttttgtc tatttttaaa 480

cttgaaagaa acaacagccc agatttcaaa aataatataa tgcacttata cctaaaaaaa 540

caaccaggag tgcccagtta ataacatttt ttaaatgtgg ggatgggaag ggcattagag 600

gagtcttcct tctattgaag attcattaaa gtatttaaga tatgcccttt cactctttat 660

ataaatccaa gatttttctt tgctgaagta tttaaaactt ttgtaccttt atatgtagat 720

atgaatttga aaatatgctt atgtgta 747

<210> 34
<211> 2021
<212> DNA
<213> Murinae gen. sp.

<400> 34
gggcaagaaa cttcaacaga agtccacacc tccccagaag catccgtcaa agagggacga 60

gcagaccgag caaacactcc cagcgccaaa gatcgggact gtggggaatc tgcagggccc 120

agttccaagc tctctgggaa ccggaacggc agggaaagcc gagcgggcgg cctgaaggag 180

agaagcaatg gatcagaggg ggctccaagt gaaggaaggg taagtccaaa gagcagcgtt 240

cctgagactg gcctgataga ctgcagcact tcacaggccg ccagttctcc agaaccaacc 300

agcctcaagg gctccacatc tctgcctgtt cactcagctt ccagagctag gaaagagcag 360

ggtgctggca gccattccga cgcttgaaga aaactgtctc gttcccccag aagcacatgt 420

atgttacact ggagatgacc aactgatttg tcttataaag gccactgttg agctgggaga 480

gtagcccagt ggtacagcgc ccacctggaa tacttgagga cctggggttg tctcccagca 540

ctgcaaaagg aaaattcact gttacagtct tccttgcact taaaccagct ttgtctattg 600

ttttttggt ttggctttta tttttgttgc tgttattttt gttgttgttt gtttgttttt 660

ttgtttgttt gtttgagaca gggtttcttt gctagccctg actgtcctga aactccctct 720

gtagaccagg ctggcctcaa acttacagag atctgcctgc ctcagcctcc cgagtgctgg 780

gaataatggt gtggtcacca ctgcccagcc ttttgtctgt ttttaaactt gaaagaaaca 840

acagcccaga tttcaaaaat aatataatgc atttatacct aaaaaaccaa ccaggagtgc 900

ccagttaata acacttttta aatgtgggga tgggaagggc attagaggag tcttccttct 960

attgaagatt cattaaagta ttttaagata tgctctttca ctctttatat aaatccaaga 1020

tttttctttg ctgaagtatt taaaactttt gtacctttat atgtagatat gaatttgaaa 1080

atatgcttat gtgtatttga acttttgaaa atcctagaga attgaatcaa atatttttat 1140

gatgtttttc tactatttta gctactttgc gactgtgata gctgttacac tggatttta 1200

aaaaacttgt acagcagcct ctttacagta aaaagagtgg gtgtcacact gaaaggtctg 1260

taagaagtgg tcacagccac ccctaccttc cccaaaagga ggaacttggt ggcaggtccc 1320

tccctgattg gactgtccct ttctttctgc atgttataaa tcagcaggta agatggtagg 1380

tttttacaag ttaggccgag ctgtcgattc ccctttaag tgttgaatta ggattgaatt 1440

atggccattt gtagttgctc gtgcctgtct ttattttagt attttatttc ccgagacagg 1500

aactcactgt gtggtgctcc ttggctgtct ggtgttcagt ctgtcccagg caggtcacag 1560

agatctcccc ctctgcagcc cactcatctc tcccaagcca ccacactcag cttttatctg 1620

ttttaaaaat ttaaacttaa aaaaatgttt ttggaatagt acaaacacat tgtgttgtaa 1680

atttctttga tgctatgcaa aattcctatc tgcatctaag cctgcaaaag aaaatgtgcg 1740

aagggcagag tcagagttgg gcaggaagag tgtagtgcag cagatgcagc gtgaagacac 1800

tgaaggtgct aagacagcgt ctcagtgctg gtcctcctta aggattatct cgccagcgag 1860

gttttcttag atactttgat cccattggag ctctgttaaa gtttaaaatg aaaattatca 1920

tgtactgtat gggaaatgta aatactaact tttccacata tgtaaacttc agacacaaat 1980

ttttttgtgt gttcttttca tcaataaaat tttctttgta t 2021

<210> 35
<211> 709
<212> PRT
<213> Murinae gen. sp.

<400> 35

Met Glu Arg Ser Pro Phe Leu Leu Ala Cys Ile Leu Leu Pro Leu Val
1 5 10 15

Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
20 25 30

Met Lys Met Thr Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
35 40 45

Tyr Asp Gln Gly Ile Ala Ala Val Glu Met Gly His Phe Leu His Leu

```
    50                  55                  60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Met Phe Leu Cys Gln Ala
65                  70                  75                  80

Phe Ile Pro Thr Cys Thr Glu Gln Ile His Val Val Leu Pro Cys Arg
                85                  90                  95

Lys Leu Cys Glu Lys Ile Val Ser Asp Cys Lys Lys Leu Met Asp Thr
            100                 105                 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asn Arg Leu Pro His
        115                 120                 125

Cys Asp Asp Thr Val Pro Val Thr Ser His Pro His Thr Glu Leu Ser
    130                 135                 140

Gly Pro Gln Lys Lys Ser Asp Gln Val Pro Arg Asp Ile Gly Phe Trp
145                 150                 155                 160

Cys Pro Lys His Leu Arg Thr Ser Gly Asp Gln Gly Tyr Arg Phe Leu
                165                 170                 175

Gly Ile Glu Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
            180                 185                 190

Asp Glu Leu Asp Phe Ala Lys Ser Phe Ile Gly Ile Val Ser Ile Phe
        195                 200                 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
    210                 215                 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225                 230                 235                 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Val Gly Phe Leu Leu Gly Asn
                245                 250                 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
            260                 265                 270

Val Val Leu Gly Ser Lys Asn Lys Ala Cys Ser Val Val Phe Met Phe
        275                 280                 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
    290                 295                 300
```

```
Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305                 310                 315                 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Ala Pro Gly
                325                 330                 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
            340                 345                 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
        355                 360                 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
    370                 375                 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385                 390                 395                 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
                405                 410                 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
            420                 425                 430

Gly Cys Tyr Val Tyr Glu Leu Val Asn Arg Ile Thr Trp Glu Met Thr
        435                 440                 445

Trp Phe Ser Asp His Cys His Gln Tyr Arg Ile Pro Cys Pro Tyr Gln
    450                 455                 460

Ala Asn Pro Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
465                 470                 475                 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
                485                 490                 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
            500                 505                 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
        515                 520                 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Gly
    530                 535                 540

Ala Pro Gly Pro His Arg Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545                 550                 555                 560
```

```
Ser Thr Gly Ala Thr Thr Asn His Gly Thr Ser Ala Met Ala Ile Ala
                565                 570                 575

Asp His Asp Tyr Leu Gly Gln Glu Thr Ser Thr Glu Val His Thr Ser
            580                 585                 590

Pro Glu Ala Ser Val Lys Glu Gly Arg Ala Asp Arg Ala Asn Thr Pro
        595                 600                 605

Ser Ala Lys Asp Arg Asp Cys Gly Glu Ser Ala Gly Pro Ser Ser Lys
    610                 615                 620

Leu Ser Gly Asn Arg Asn Gly Arg Glu Ser Arg Ala Gly Gly Leu Lys
625                 630                 635                 640

Glu Arg Ser Asn Gly Ser Glu Gly Ala Pro Ser Glu Gly Arg Val Ser
                645                 650                 655

Pro Lys Ser Ser Val Pro Glu Thr Gly Leu Ile Asp Cys Ser Thr Ser
            660                 665                 670

Gln Ala Ala Ser Ser Pro Glu Pro Thr Ser Leu Lys Gly Ser Thr Ser
        675                 680                 685

Leu Pro Val His Ser Ala Ser Arg Ala Arg Lys Glu Gln Gly Ala Gly
    690                 695                 700

Ser His Ser Asp Ala
705
```

<210> 36
<211> 2039
<212> DNA
<213> Homo sapiens

<400> 36

```
aggagacaac attagtggag tttgctttgt tggcctttat gacctggatg cttctcgcta     60

ctttgtactc ttgccactgt gcctttgtgt gtttgttggg ctctctcttc ttttagctgg    120

cattatttcc ttaaatcatg ttcgacaagt catacaacat gatggccgga accaagaaaa    180

actaaagaaa tttatgattc gaattggagt cttcagcggc ttgtatcttg tgccattagt    240

gacacttctc ggatgttacg tctatgagca agtgaacagg attacctggg agataacttg    300

ggtctctgat cattgtcgtc agtaccatat cccatgtcct tatcaggcaa aagcaaaagc    360

tcgaccagaa ttggctttat ttatgataaa atacctgatg acattaattg ttggcatctc    420

tgctgtcttc tgggttggaa gcaaaaagac atgcacagaa tgggctgggt tttttaaacg    480
```

aaatcgcaag agagatccaa tcagtgaaag tcgaagagta ctacaggaat catgtgagtt 540

tttcttaaag cacaattcta aagttaaaca caaaaagaag cactataaac caagttcaca 600

caagctgaag gtcatttcca aatccatggg aaccagcaca ggagctacag caaatcatgg 660

cacttctgca gtagcaatta ctagccatga ttacctagga caagaaactt tgacagaaat 720

ccaaacctca ccagaaacat caatgagaga ggtgaaagcg gacggagcta gcacccccag 780

gttaagagaa caggactgtg gtgaacctgc ctcgccagca gcatccatct ccagactctc 840

tggggaacag gtcgacggga agggccaggc aggcagtgta tctgaaagtg cgcggagtga 900

aggaaggatt agtccaaaga gtgatattac tgacactggc ctggcacaga gcaacaattt 960

gcaggtcccc agttcttcag aaccaagcag cctcaaaggt tccacatctc tgcttgttca 1020

cccggtttca ggagtgagaa aagagcaggg aggtggttgt cattcagata cttgaagaac 1080

attttctctc gttactcaga agcaaatttg tgttacactg gaagtgacct atgcactgtt 1140

ttgtaagaat cactgttaca ttcttctttt gcacttaaag ttgcattgcc tactgttata 1200

ctggaaaaaa tagagttcaa gaataatatg actcatttca cacaaaggtt aatgacaaca 1260

atatacctga aaacagaaaa tgtgcaggtt aataatattt ttttaatagt gtgggaggac 1320

agagttagag gaatcttcct tttctattta tgaagattct actcttggta agagtatttt 1380

aagatgtact atgctatttt acttttttga tataaaatca agatatttct ttgctgaagt 1440

atttaaatct tatccttgta tcttttttata catatttgaa aataagctta tatgtatttg 1500

aacttttttg aaatcctatt caagtatttt tatcatgcta ttgtgatatt ttagcacttt 1560

ggtagctttt acactgaatt tctaagaaaa ttgtaaaata gtcttctttt atactgtaaa 1620

aaaagatata ccaaaaagtc ttataatagg aatttaactt taaaaaccca cttattgata 1680

ccttaccatc taaaatgtgt gatttttata gtctcgtttt aggaatttca cagatctaaa 1740

ttatgtaact gaaataaggt gcttactcaa agagtgtcca ctattgattg tattatgctg 1800

ctcactgatc cttctgcata tttaaaataa aatgtcctaa agggttagta gacaaaatgt 1860

tagtcttttg tatattaggc caagtgcaat tgacttccct tttttaatgt ttcatgacca 1920

cccattgatt gtattataac cacttacagt tgcttatatt ttttgtttta acttttgttt 1980

tttaacattt agaatattac attttgtatt atacagtacc tttctcagac attttgtag 2039

<210> 37
<211> 706
<212> PRT
<213> Homo sapiens

<400> 37

Met Glu Met Phe Thr Phe Leu Leu Thr Cys Ile Phe Leu Pro Leu Leu
1 5 10 15

```
Arg Gly His Ser Leu Phe Thr Cys Glu Pro Ile Thr Val Pro Arg Cys
            20                  25                  30

Met Lys Met Ala Tyr Asn Met Thr Phe Phe Pro Asn Leu Met Gly His
        35                  40                  45

Tyr Asp Gln Ser Ile Ala Ala Val Glu Met Glu His Phe Leu Pro Leu
    50                  55                  60

Ala Asn Leu Glu Cys Ser Pro Asn Ile Glu Thr Phe Leu Cys Lys Ala
65                  70                  75                  80

Phe Val Pro Thr Cys Ile Glu Gln Ile His Val Val Pro Pro Cys Arg
                85                  90                  95

Lys Leu Cys Glu Lys Val Tyr Ser Asp Cys Lys Lys Leu Ile Asp Thr
            100                 105                 110

Phe Gly Ile Arg Trp Pro Glu Glu Leu Glu Cys Asp Arg Leu Gln Tyr
        115                 120                 125

Cys Asp Glu Thr Val Pro Val Thr Phe Asp Pro His Thr Glu Phe Leu
    130                 135                 140

Gly Pro Gln Lys Lys Thr Glu Gln Val Gln Arg Asp Ile Gly Phe Trp
145                 150                 155                 160

Cys Pro Arg His Leu Lys Thr Ser Gly Gly Gln Gly Tyr Lys Phe Leu
                165                 170                 175

Gly Ile Asp Gln Cys Ala Pro Pro Cys Pro Asn Met Tyr Phe Lys Ser
            180                 185                 190

Asp Glu Leu Glu Phe Ala Lys Ser Phe Ile Gly Thr Val Ser Ile Phe
        195                 200                 205

Cys Leu Cys Ala Thr Leu Phe Thr Phe Leu Thr Phe Leu Ile Asp Val
    210                 215                 220

Arg Arg Phe Arg Tyr Pro Glu Arg Pro Ile Ile Tyr Tyr Ser Val Cys
225                 230                 235                 240

Tyr Ser Ile Val Ser Leu Met Tyr Phe Ile Gly Phe Leu Leu Gly Asp
                245                 250                 255

Ser Thr Ala Cys Asn Lys Ala Asp Glu Lys Leu Glu Leu Gly Asp Thr
            260                 265                 270
```

```
Val Val Leu Gly Ser Gln Asn Lys Ala Cys Thr Val Leu Phe Met Leu
        275                 280                 285

Leu Tyr Phe Phe Thr Met Ala Gly Thr Val Trp Trp Val Ile Leu Thr
    290                 295                 300

Ile Thr Trp Phe Leu Ala Ala Gly Arg Lys Trp Ser Cys Glu Ala Ile
305                 310                 315                 320

Glu Gln Lys Ala Val Trp Phe His Ala Val Ala Trp Gly Thr Pro Gly
                325                 330                 335

Phe Leu Thr Val Met Leu Leu Ala Met Asn Lys Val Glu Gly Asp Asn
            340                 345                 350

Ile Ser Gly Val Cys Phe Val Gly Leu Tyr Asp Leu Asp Ala Ser Arg
        355                 360                 365

Tyr Phe Val Leu Leu Pro Leu Cys Leu Cys Val Phe Val Gly Leu Ser
    370                 375                 380

Leu Leu Leu Ala Gly Ile Ile Ser Leu Asn His Val Arg Gln Val Ile
385                 390                 395                 400

Gln His Asp Gly Arg Asn Gln Glu Lys Leu Lys Lys Phe Met Ile Arg
                405                 410                 415

Ile Gly Val Phe Ser Gly Leu Tyr Leu Val Pro Leu Val Thr Leu Leu
            420                 425                 430

Gly Cys Tyr Val Tyr Glu Gln Val Asn Arg Ile Thr Trp Glu Ile Thr
        435                 440                 445

Trp Val Ser Asp His Cys Arg Gln Tyr His Ile Pro Cys Pro Tyr Gln
    450                 455                 460

Ala Lys Ala Lys Ala Arg Pro Glu Leu Ala Leu Phe Met Ile Lys Tyr
465                 470                 475                 480

Leu Met Thr Leu Ile Val Gly Ile Ser Ala Val Phe Trp Val Gly Ser
                485                 490                 495

Lys Lys Thr Cys Thr Glu Trp Ala Gly Phe Phe Lys Arg Asn Arg Lys
            500                 505                 510

Arg Asp Pro Ile Ser Glu Ser Arg Arg Val Leu Gln Glu Ser Cys Glu
```

515 520 525

Phe Phe Leu Lys His Asn Ser Lys Val Lys His Lys Lys Lys His Tyr
530 535 540

Lys Pro Ser Ser His Lys Leu Lys Val Ile Ser Lys Ser Met Gly Thr
545 550 555 560

Ser Thr Gly Ala Thr Ala Asn His Gly Thr Ser Ala Val Ala Ile Thr
565 570 575

Ser His Asp Tyr Leu Gly Gln Glu Thr Leu Thr Glu Ile Gln Thr Ser
580 585 590

Pro Glu Thr Ser Met Arg Glu Val Lys Ala Asp Gly Ala Ser Thr Pro
595 600 605

Arg Leu Arg Glu Gln Asp Cys Gly Glu Pro Ala Ser Pro Ala Ala Ser
610 615 620

Ile Ser Arg Leu Ser Gly Glu Gln Val Asp Gly Lys Gly Gln Ala Gly
625 630 635 640

Ser Val Ser Glu Ser Ala Arg Ser Glu Gly Arg Ile Ser Pro Lys Ser
645 650 655

Asp Ile Thr Asp Thr Gly Leu Ala Gln Ser Asn Asn Leu Gln Val Pro
660 665 670

Ser Ser Ser Glu Pro Ser Ser Leu Lys Gly Ser Thr Ser Leu Leu Val
675 680 685

His Pro Val Ser Gly Val Arg Lys Glu Gln Gly Gly Gly Cys His Ser
690 695 700

Asp Thr
705

<210> 38
<211> 773
<212> DNA
<213> Murinae gen. sp.

<400> 38
ctgaggtgct agcaccagcc tggttgtctc tggcgggcct gaagcaagca tggatcaaga 60

ggctgtgggc aacgttgtgc tcctggccct tgtcaccctc atcagcgtgg tccagaatgc 120

gttctttgcc cacaaggtgg agcatgaaag caaggcgcat aatgggagaa gcttccagag 180

gaccgggact cttgcctttg agcgggtcta cactgccaac cagaactgcg tagatgcgta 240

ccccactttc cttgtggtac tctggactgc aggactactt tgcagccaag tccctgcagc 300

cttcgccgga ctgatgtacc tgtttgtgag gcaaaaatac tttgtcggct atctgggaga 360

gagaactcag agcacccctg gctacatctt cggcaagcgg atcatcctgt tcctgttcct 420

catgtccttc gccgggatac tcaaccatta cctcatcttc ttcttcggaa gcgactttga 480

gaactacatc agaacggtaa gcacgacgat ctccccgctg cttctcatcc cctgattgct 540

ggagacagag aaggacgctc accagatcaa tagagacgca tcataacgca acgccgcgaa 600

ggcttctgct cctcttcaag ctgtagatgc tgtcaatctt gctgccctcg gggctctgtg 660

gcatccgtta actttgcttt tccgggaaga aaaatgtctt gtgctaagct ccacccctcg 720

aatgcggcgg tgggccagga tttatgtcta catccagcct atacttctcc tgg 773

<210> 39
<211> 852
<212> DNA
<213> Murinae gen. sp.

<400> 39
ggaaggctga ggtgctagca ccagcctggt tgtctctggc gggcctgaag caagcatgga 60

tcaagaggct gtgggcaacg ttgtgctcct ggcccttgtc accctcatca gcgtggtcca 120

gaatgtgttt tttgcccact atgtggagca tgaaagcaat gcgcataatg ggagaagctt 180

ccagaggacc gggactcttg cctttgagcg ggtctacact gccaaccaga actgcgtaga 240

tgcgtacccc actttccttg tggtactctg gactgcagga ctactttgca gccaagtccc 300

tgccgccttc gccggactga tgtacctgtt tgtgaggcaa aaatactttg tcggctatct 360

gggagagaga actcagagca cccctggcta catcttcggc aagcggatca tcctgttcct 420

gttcctcatg tccttcgccg ggatactcaa ccattacctc atcttcttct tcggaagcga 480

ctttgagaac tacatcagaa cggtaagcac gacgatctcc ccgctgcttc tcatcccctg 540

attgctggag acagagaagg acgctcacca gatcaataga gacgcatcat aacgcaacgc 600

cgcgaaggct tctgctcctc ttcaagctgt agatgctgtc aatcttgctg ccctcggggc 660

tctgtggcat ccgttaactt tgcttttccg ggaagaaaaa tgtcttgtgc tagctccacc 720

cctcgaatgc ggcggtggcc caggatttat tgtctacatc cagcctatac ttctcctggc 780

ttatcctgct ttctgaagat gtcttgtaat cagacacgtg ttttcctaaa ataaagggta 840

tagacaaaat tt 852

<210> 40
<211> 161
<212> PRT
<213> Murinae gen. sp.

<400> 40

Met Asp Gln Glu Ala Val Gly Asn Val Val Leu Leu Ala Leu Val Thr
1 5 10 15

Leu Ile Ser Val Val Gln Asn Val Phe Phe Ala His Tyr Val Glu His
20 25 30

Glu Ser Asn Ala His Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
50 55 60

Pro Thr Phe Leu Val Val Leu Trp Thr Ala Gly Leu Leu Cys Ser Gln
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
85 90 95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Phe Ala
115 120 125

Gly Ile Leu Asn His Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
130 135 140

Asn Tyr Ile Arg Thr Val Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
145 150 155 160

Pro

<210> 41
<211> 873
<212> DNA
<213> Homo sapiens

<400> 41
acttcccctt cctgtacagg gcaggttgtg cagctggagg cagagcagtc ctctctgggg 60

agcctgaagc aaacatggat caagaaactg taggcaatgt tgtcctgttg gccatcgtca 120

ccctcatcag cgtggtccag aatggattct ttgcccataa agtggagcac gaaagcagga 180

cccagaatgg gaggagcttc cagaggaccg gaacacttgc ctttgagcgg gtctacactg 240

ccaaccagaa ctgtgtagat gcgtacccca ctttcctcgc tgtgctctgg tctgcggggc 300

tactttgcag ccaagttcct gctgcgtttg ctggactgat gtacttgttt gtgaggcaaa 360

agtactttgt cggttaccta ggagagagaa cgcagagcac ccctggctac atatttggga 420

aacgcatcat actcttcctg ttcctcatgt ccgttgctgg catattcaac tattacctca 480

tcttcttttt cggaagtgac tttgaaaact acataaagac gatctccacc accatctccc 540

ctctacttct cattccctaa ctctctgctg aatatggggt tggtgttctc atctaatcaa 600

tacctacaag tcatcataat tcagctcttg agagcattct gctcttcttt agatggctgt 660

aaatctattg gccatctggg cttcacagct tgagttaacc ttgcttttcc gggaacaaaa 720

tgatgtcatg tcagctccgc cccttgaaca tgaccgtggc cccaaatttg ctattcccat 780

gcattttgtt tgtttcttca cttatcctgt tctctgaaga tgttttgtga ccaggtttgt 840

gttttcttaa aataaaatgc agagacatgt ttt 873

<210> 42
<211> 161
<212> PRT
<213> Homo sapiens

<400> 42

Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile Val Thr
1 5 10 15

Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val Glu His
20 25 30

Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu
35 40 45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr
50 55 60

Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys Ser Gln
65 70 75 80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys
85 90 95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Val Ala
115 120 125

Gly Ile Phe Asn Tyr Tyr Leu Ile Phe Phe Phe Gly Ser Asp Phe Glu
130 135 140

Asn Tyr Ile Lys Thr Ile Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile
145 150 155 160

Pro

<210> 43
<211> 803
<212> DNA
<213> Murinae gen. sp.

<400> 43
ttcagcttta tgggttggct tccttgactg cattttctgt cagttaacta aactccagac 60

tcatggattt tctcgaccag aaaatcagac tattttcctg aataatctac tagaaacttt 120

tacggaacac atttcatgtt tcctttgaag agttaagaga agaaagtatt tgtaagaaca 180

ggaaaagaaa caaatacttt gcaaataaac tggctgctgc tgtgaccaca tctgaatagc 240

aaaggcgatc gatcaagcgc tgcggacaaa aggcctcctg taagctgcac tgcctgacaa 300

tggtaagctc caatggctcc cagtgccctt atgacgactc ctttaagtac actctgtacg 360

ggtgcatgtt cagcatggtc ttcgtgcttg ggctgatatc caactgtgtt gcgatataca 420

ttttcatctg tgccctcaaa gtgagaaatg aaactacaac gtacatgatt aacctggcaa 480

tgtcagattt acttttcgtc tttactttgc catttcggat tttttacttt gcaacacgga 540

attggccatt tggagatcta ctctgtaaga tttcagtaat gctgttttac accaatatgt 600

atgggaagca ttctgttctt aacctgtatc agtgtagatc gatttctggc aattgtctac 660

ccatttaagt caaagacttt aagaaacgaa acgaaaatgc aaagaatcgt ttgcattgcc 720

tgtgtggttc acagtgatgg gaggaagtgc gctgcagttt tctttcagtc gacccactct 780

caggggaaca atactcagaa gct 803

<210> 44
<211> 1849
<212> DNA
<213> Murinae gen. sp.

<400> 44
agagacagcc catctcacaa tacagctggc aacctccgaa aggcctctcc attcagcaag 60

cgcgaacatg cttaggaatt tatctgggat cccttaaacg actgcctatc gccgtccgga 120

atcaatgtag aaatacaaag tttgagaata aaaagaagga agaagtaccc gaggacgacg 180

ggcggacgga cgcacggcga gtgtttgtga ctgaagtaaa gctggtttgg accctggcgg 240

ctgaagcaca agtttccacg cggactggtc tggtccgact tggaacagtt tttccttaca 300

ctttcagctt tatgggttgg cttccttgac tgcattttct gtcagttaac taaactccag 360

actcatggat tttctcgacc agaaaatcag actattttcc tgaataatct actagaaact 420

tttacggaac acatttcatg tttcctttga agagttaaga gaagaaagta tttgtaagaa 480

caggaaaaga aacaaatact ttgcaaataa actggctgct gctgtgacca catctgaata 540

gcaaaggcga tcgatcaagc gctgcggaca aaaggcctcc tgtaagctgc actgcctgac 600

aatggtaagc tccaatggct cccagtgccc ttatgacgac tcctttaagt acactctgta 660

cgggtgcatg ttcagcatgg tcttcgtgct tgggctgata tccaactgtg ttgcgatata 720

cattttcatc tgtgccctca aagtgagaaa tgaaactaca acgtacatga ttaacctggc 780

aatgtcagat ttacttttcg tctttacttt gccatttcgg atttttact ttgcaacacg 840

gaattggcca tttggagatc tactctgtaa gatttcagta atgctgtttt acaccaatat 900

gtatggaagc attctgttct taacctgtat cagtgtagat cgatttctgg caattgtcta 960

cccatttaag tcaaagactt taagaacgaa acgaaatgca aagatcgttt gcattgctgt 1020

gtggttcaca gtgatgggag gaagtgcgcc tgcagttttc tttcagtcga cccactctca 1080

ggggaacaat acctcagaag cctgctttga gaactttcca gcggccacat ggaaaactta 1140

tctctccagg attgtgattt tcattgaaat agtgggcttt tttatccctc tcattttgaa 1200

cgtaacttgt tctagtatgg tgctaagaac tttaaataaa cctgttacat taagtagaag 1260

caaaatgaac aaaactaagg ttttaaaaat gatttttgtc cacttggtca tcttctgttt 1320

ctgttttgtg ccctacaaca tcaacctcat tttgtactcg ctcatgagga cacagacctt 1380

tgttaactgc tctgtggtgg cggcagtgag gaccatgtac ccgatcactc tctgcatcgc 1440

tgtttccaac tgctgctttg accctattgt ttactacttc acctcagaca caattcagaa 1500

ctcaataaaa atgaaaaact ggtcggttag aagaagtgac tccaggttct ctgaagttca 1560

gggcactgag aattttatcc aacacaacct acagacctta aaaaataaga tatttgataa 1620

tgaatctgca atataagctg cctgactaag ccactgggac tgctccgtgt tcaactgtga 1680

aaactgtgtt cttgggaact atctctccgg ctccaacaga aaatattttt aaaggaagtt 1740

tgtgtctgat gtgttaaaca ttaaaatata ttctattctt gtatgcacgc cattttactt 1800

tcttgaacca ctttaacgtg ttttttcctc attaaaaaaa aaaaactcc 1849

<210> 45
<211> 316
<212> PRT
<213> Murinae gen. sp.

<400> 45

Asp Asp Ser Phe Lys Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val
1 5 10 15

Phe Val Leu Gly Leu Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile
20 25 30

```
Cys Ala Leu Lys Val Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu
        35                  40                  45

Ala Met Ser Asp Leu Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe
    50                  55                  60

Tyr Phe Ala Thr Arg Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile
65                  70                  75                  80

Ser Val Met Leu Phe Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu
                85                  90                  95

Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys
            100                 105                 110

Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala Lys Ile Val Cys Ile Ala
        115                 120                 125

Val Trp Phe Thr Val Met Gly Gly Ser Ala Pro Ala Val Phe Phe Gln
    130                 135                 140

Ser Thr His Ser Gln Gly Asn Asn Thr Ser Glu Ala Cys Phe Glu Asn
145                 150                 155                 160

Phe Pro Ala Ala Thr Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe
                165                 170                 175

Ile Glu Ile Val Gly Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys
            180                 185                 190

Ser Ser Met Val Leu Arg Thr Leu Asn Lys Pro Val Thr Leu Ser Arg
        195                 200                 205

Ser Lys Met Asn Lys Thr Lys Val Leu Lys Met Ile Phe Val His Leu
    210                 215                 220

Val Ile Phe Cys Phe Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu
225                 230                 235                 240

Tyr Ser Leu Met Arg Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala
                245                 250                 255

Ala Val Arg Thr Met Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn
            260                 265                 270

Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln
        275                 280                 285
```

Asn Ser Ile Lys Met Lys Asn Trp Ser Val Arg Arg Ser Asp Ser Arg
290 295 300

Phe Ser Glu Val Gln Gly Thr Glu Asn Phe Ile Gln
305 310 315

<210> 46
<211> 1035
<212> DNA
<213> Homo sapiens

<400> 46
atggtaagcg ttaacagctc ccactgcttc tataatgact cctttaagta cactttgtat 60

gggtgcatgt tcagcatggt gtttgtgctt gggttaatat ccaattgtgt tgccatatac 120

attttcatct gcgtcctcaa agtccgaaat gaaactacaa cttacatgat taacttggca 180

atgtcagact tgctttttgt ttttacttta cccttcagga ttttttactt cacaacacgg 240

aattggccat ttggagattt actttgtaag atttctgtga tgctgtttta taccaacatg 300

tacggaagca ttctgttctt aacctgtatt agtgtagatc gatttctggc aattgtctac 360

ccatttaagt caaagactct aagaaccaaa agaaatgcaa agattgtttg cactggcgtg 420

tggttaactg tgatcggagg aagtgcaccc gccgtttttg ttcagtctac ccactctcag 480

ggtaacaatg cctcagaagc ctgctttgaa aattttccag aagccacatg gaaaacatat 540

ctctcaagga ttgtaatttt catcgaaata gtgggatttt ttattcctct aattttaaat 600

gtaacttgtt ctagtatggt gctaaaaact ttaaccaaac ctgttacatt aagtagaagc 660

aaaataaaca aaactaaggt tttaaaaatg atttttgtac atttgatcat attctgtttc 720

tgttttgttc cttacaatat caatcttatt ttatattctc ttgtgagaac acaaacattt 780

gttaattgct cagtagtggc agcagtaagg acaatgtacc caatcactct ctgtattgct 840

gtttccaact gttgttttga ccctatagtt tactacttta catcggacac aattcagaat 900

tcaataaaaa tgaaaaactg gtctgtcagg agaagtgact tcagattctc tgaagttcat 960

ggtgcagaga attttattca gcataaccta cagaccttaa aaagtaagat atttgacaat 1020

gaatctgctg cctga 1035

<210> 47
<211> 344
<212> PRT
<213> Homo sapiens

<400> 47

Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys
1 5 10 15

```
Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val Phe Val Leu Gly Leu
            20                  25                  30

Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val
        35                  40                  45

Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu
    50                  55                  60

Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg
65                  70                  75                  80

Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe
                85                  90                  95

Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val
            100                 105                 110

Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg
        115                 120                 125

Thr Lys Arg Asn Ala Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val
    130                 135                 140

Ile Gly Gly Ser Ala Pro Ala Val Phe Val Gln Ser Thr His Ser Gln
145                 150                 155                 160

Gly Asn Asn Ala Ser Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr
                165                 170                 175

Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly
            180                 185                 190

Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu
        195                 200                 205

Lys Thr Leu Thr Lys Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys
    210                 215                 220

Thr Lys Val Leu Lys Met Ile Phe Val His Leu Ile Ile Phe Cys Phe
225                 230                 235                 240

Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg
                245                 250                 255

Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala Ala Val Arg Thr Met
            260                 265                 270
```

```
Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro
        275                 280                 285

Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met
    290                 295                 300

Lys Asn Trp Ser Val Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His
305                 310                 315                 320

Gly Ala Glu Asn Phe Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys
                325                 330                 335

Ile Phe Asp Asn Glu Ser Ala Ala
            340
```

<210> 48
<211> 814
<212> DNA
<213> Murinae gen. sp.

<400> 48
gagcgcgcgt aagatggcac taccattttc tgtcaacctt cggggtgcgt aatggcctct 60

ggccaggcct agcacatgta cctcacagac caactggcaa gcagccttca gggagctcga 120

tccccaaaca gccagtcacc acctctgtcc cctcttcact gttggtcgtc agactgcctg 180

agtggacagc aggctggtcg cgttgtattt tcacttcctt cctctgactg gcttgctctt 240

gtctctcagt ctttcatccc aggcagctgc ctgaggtagg tgaggaggat ggtgagccag 300

gcaggtctac aataaaggca gctctgtccg gctccttctg gctcgtgagt gtcaccggcc 360

tggaagactg agggaatggc tcccctctct cctccccgtc tttccccagt tccttcccta 420

tgttggccca tgtgcccagg gagttggaag catcagggag accctcttag tgtggggaag 480

gaagtcagag accattgaca cagtgaagag gcaggatcat gtgttggaag cctgttagca 540

ggaccaaggt gactcttggg agagactctt gtggacacag gccgtggtgg cttgtcagac 600

cttaaagggt ccaggcccac ccctgccagg atccctggtc tgctttctcc aggacacact 660

gggacactgc tgagtaatga gcagcttatt acacacaatg ggaagagggg cagagagggc 720

tgtgtcggtt gagtctcggc tgggactgaa gtttgccata agtagtggtt gtacatccag 780

gagcctggct acctgtcttt acccccttgaa ggac 814

<210> 49
<211> 1164
<212> DNA
<213> Murinae gen. sp.

<400> 49

ggtcgctatt tcttggtgcg tgacatcacc gagaagatgg acatactggg caccttgaag 60

agctgtgggg ctcccaactt ccggcaggtg cggggaggcc tccctgtgtt tggcatggga 120

cagcccagcc tcttggggtt caggagggtc ctgcagaaac tccagacgga cggactcaag 180

gagtgcatta tcttctgcgt gcgggaggag cctgtggtgt tcttgcgcgc tgaggaggac 240

tttgtgtctt acacacctcg agacaaggag agccttcatg agaacctcag ggaccctagt 300

ccaggggtca aggctgagaa tctggagctg gccatccaga aagagatcca tgactttgcc 360

caattgagag ataatgtgta ccacgtatac cacaacacag aggacctgcg cggggagccg 420

cacaccgtgg ccatccgagg tgaggatggc gtgtgcgtga ccgaggaggt gtttaagcgg 480

ccgctcttcc tgcagcccac ctacagatac caccgcctcc ccttgccaga gcaaggggcc 540

cccctggaag cccagtttga tgcctttgtc agcgttcttc gggagacccc cagccttctg 600

ccactcagag ataaccacgg gcctctgcct gccctcctgt tcagctgcca gtcaggtgta 660

ggcagaacca acctaggcat ggtcctggga accctcgtca tgttccacca cagtaggacc 720

acctcccagc tagaggcagc ctccccgttg gccaaacccc tgcccatgga gcagtttcag 780

gtgatccagg gcttcatctg taaggtgcca caggggaaga aaatggtgga ggaggtggat 840

cgagcgatca gtgcctgtgc agagttgcat gacctgaagg aggaggtcct aaaaaaccag 900

aggaggctgg aaagcttcag gccagagagc cggggacagg aatgtggtag tcagcaagct 960

gtccagcaga gggcgctgtg gagcctggag ctgtacttct atctgctcct atttaactac 1020

tatctgcatg agcagtaccc cctggccttt gccctcagtt tcagtcgatg gctgtgtacc 1080

catcctgagc tgtaccgtct gctggtggag ctgaattcag tggggccctt ggtccctggg 1140

gacctcatcg ccaagggctc cctg 1164

<210> 50
<211> 388
<212> PRT
<213> Murinae gen. sp.

<400> 50

Gly Arg Tyr Phe Leu Val Arg Asp Ile Thr Glu Lys Met Asp Ile Leu
1 5 10 15

Gly Thr Leu Lys Ser Cys Gly Ala Pro Asn Phe Arg Gln Val Arg Gly
20 25 30

Gly Leu Pro Val Phe Gly Met Gly Gln Pro Ser Leu Leu Gly Phe Arg
35 40 45

Arg Val Leu Gln Lys Leu Gln Thr Asp Gly Leu Lys Glu Cys Ile Ile
50 55 60

```
Phe Cys Val Arg Glu Glu Pro Val Val Phe Leu Arg Ala Glu Glu Asp
65                  70                  75                  80

Phe Val Ser Tyr Thr Pro Arg Asp Lys Glu Ser Leu His Glu Asn Leu
                85                  90                  95

Arg Asp Pro Ser Pro Gly Val Lys Ala Glu Asn Leu Glu Leu Ala Ile
            100                 105                 110

Gln Lys Glu Ile His Asp Phe Ala Gln Leu Arg Asp Asn Val Tyr His
        115                 120                 125

Val Tyr His Asn Thr Glu Asp Leu Arg Gly Glu Pro His Thr Val Ala
    130                 135                 140

Ile Arg Gly Glu Asp Gly Val Cys Val Thr Glu Glu Val Phe Lys Arg
145                 150                 155                 160

Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His Arg Leu Pro Leu Pro
                165                 170                 175

Glu Gln Gly Ala Pro Leu Glu Ala Gln Phe Asp Ala Phe Val Ser Val
            180                 185                 190

Leu Arg Glu Thr Pro Ser Leu Leu Pro Leu Arg Asp Asn His Gly Pro
        195                 200                 205

Leu Pro Ala Leu Leu Phe Ser Cys Gln Ser Gly Val Gly Arg Thr Asn
    210                 215                 220

Leu Gly Met Val Leu Gly Thr Leu Val Met Phe His His Ser Arg Thr
225                 230                 235                 240

Thr Ser Gln Leu Glu Ala Ala Ser Pro Leu Ala Lys Pro Leu Pro Met
                245                 250                 255

Glu Gln Phe Gln Val Ile Gln Gly Phe Ile Cys Lys Val Pro Gln Gly
            260                 265                 270

Lys Lys Met Val Glu Glu Val Asp Arg Ala Ile Ser Ala Cys Ala Glu
        275                 280                 285

Leu His Asp Leu Lys Glu Glu Val Leu Lys Asn Gln Arg Arg Leu Glu
    290                 295                 300

Ser Phe Arg Pro Glu Ser Arg Gly Gln Glu Cys Gly Ser Gln Gln Ala
305                 310                 315                 320
```

```
Val Gln Gln Arg Ala Leu Trp Ser Leu Glu Leu Tyr Phe Tyr Leu Leu
                325                 330                 335

Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro Leu Ala Phe Ala Leu
            340                 345                 350

Ser Phe Ser Arg Trp Leu Cys Thr His Pro Glu Leu Tyr Arg Leu Leu
        355                 360                 365

Val Glu Leu Asn Ser Val Gly Pro Leu Val Pro Gly Asp Leu Ile Ala
    370                 375                 380

Lys Gly Ser Leu
385
```

<210> 51
<211> 4303
<212> DNA
<213> Homo sapiens

<400> 51

```
ggctgctggc agactatggg tacaacggcc agcacagccc agcagacggt ctcggcaggc     60

accccatttg agggcctaca gggcagtggc acgatggaca gtcggcactc cgtcagcatc    120

cactccttcc agagcactag cttgcataac agcaaggcca agtccatcat ccccaacaag    180

gtggcccctg ttgtgatcac gtacaactgc aaggaggagt tccagatcca tgatgagctg    240

ctcaaggctc attacacgtt gggccggctc tcggacaaca cccctgagca ctacctggtg    300

caaggccgct acttcctggt gcgggatgtc actgagaaga tggatgtgct gggcaccgtg    360

ggaagctgtg gggccccaa cttccggcag gtgcagggtg ggctcactgt gttcggcatg     420

ggacagccca gcctctcagg gttcaggcgg gtcctccaga aactccagaa ggacggacat    480

agggagtgtg tcatcttctg tgtgcgggag gaacctgtgc ttttcctgcg tgcagatgag    540

gactttgtgt cctacacacc tcgagacaag cagaaccttc atgagaacct ccagggcctt    600

ggacccgggg tccgggtgga gagcctggag ctggccatcc ggaaagagat ccacgacttt    660

gcccagctga gcgagaacac ataccatgtg taccataaca ccgaggacct gtgggggggag   720

ccccatgctg tggccatcca tggtgaggac gacttgcatg tgacggagga ggtgtacaag    780

cggcccctct tcctgcagcc cacctacagg taccaccgcc tgcccctgcc cgagcaaggg    840

agtcccctgg aggcccagtt ggacgccttt gtcagtgttc tccgggagac ccccagcctg    900

ctgcagctcc gtgatgccca cgggcctccc ccagccctcg tcttcagctg ccagatgggc    960

gtgggcagga ccaacctggg catggtcctg ggcaccctca tcctgcttca ccgcagtggg   1020

accacctccc agccagaggc tgcccccacg caggccaagc ccctgcctat ggagcagttc   1080
```

caggtgatcc agagctttct ccgcatggtg ccccagggaa ggaggatggt ggaagaggtg 1140
gacagagcca tcactgcctg tgccgagttg catgacctga aagaagtggt cttggaaaac 1200
cagaagaagt tagaaggtat ccgaccggag agcccagccc agggaagcgg cagccgacac 1260
agcgtctggc agagggcgct gtggagcctg gagcgatact tctacctgat cctgtttaac 1320
tactaccttc atgagcagta cccgctggcc tttgccctca gtttcagccg ctggctgtgt 1380
gcccaccctg agctgtaccg cctgcccgtg acgctgagct cagcaggccc tgtggctccg 1440
agggacctca tcgccagggg ctccctacgg gaggacgatc tggtctcccc ggacgcgctc 1500
agcactgtca gagagatgga tgtggccaac ttccggcggg tgccccgcat gcccatctac 1560
ggcacggccc agcccagcgc caaggccctg gggagcatcc tggcctacct gacggacgcc 1620
aagaggaggc tgcggaaggt tgtctgggtg agccttcggg aggaggccgt gttggagtgt 1680
gacgggcaca cctacagcct gcggtggcct gggccccctg tggctcctga ccagctggag 1740
accctggagg cccagctgaa ggcccatcta agcgagcctc ccccaggcaa ggagggcccc 1800
ctgacctaca ggttccagac ctgccttacc atgcaggagg tcttcagcca gcaccgcagg 1860
gcctgtcctg gcctcaccta ccaccgcatc cccatgccgg acttctgtgc cccccgagag 1920
gaggactttg accagctgct ggaggccctg cgggccgccc tctccaagga cccaggcact 1980
ggcttcgtgt tcagctgcct cagcggccag ggccgtacca caactgcgat ggtggtggct 2040
gtcctggcct tctggcacat ccaaggcttc cccgaggtgg gtgaggagga gctcgtgagt 2100
gtgcctgatg ccaagttcac taagggtgaa tttcaggtag taatgaaggt ggtgcagctg 2160
ctacccgatg ggcaccgtgt gaagaaggag gtggacgcag cgctggacac tgtcagcgag 2220
accatgacgc ccatgcacta ccacctgcgg gagatcatca tctgcaccta ccgccaggcg 2280
aaggcagcga aagaggcgca agaaatgcgg aggctgcagc tgcggagcct gcagtacttg 2340
gagcgctatg tctgcctgat tctcttcaac gcgtacctcc acctggagaa ggccgactcc 2400
tggcagaggc ccttcagcac ctggatgcag gaggtggcat cgaaggctgg catctacgag 2460
atccttaacg agctgggctt ccccgagctg gagagcgggg aggaccagcc cttctccagg 2520
ctgcgctacc ggtggcagga gcagagctgc agcctcgagc cctctgcccc cgaggacttg 2580
ctgtaggggg ccttactccc tgtcccccca cccacagggc cccacgcagg cctggggtgt 2640
ctgaggtgct cttggctggg agcggccctg aggggtgctg gccttgaaat gattccccca 2700
cttcctggag agactgagcg gagttgggag ccttttttaga aagaactttt tataggacag 2760
ggagacagca cagccatccc ttgcaaacca ccaaggtgtg tggctgacct ccagggagga 2820
gcactcactg gagtgctcac aaggtgcaca ctgctgtgtg taccttgcag acaggccggc 2880
gttcagcctc caaggggctc actcccccag ttgccaaaca ctgtggatct ctctgtcctc 2940

ttctcccctc tctcagattg gcctggcagc ccctggcaca gagcagaccc ggccactggt 3000

agctccccac ttccttactc ctgctgctct gccattgccg ctccccttgt tgctgcccaa 3060

gcactgccct cgggcgtctg gcagcctgag gtgggtggag gggacagtgt tctggataga 3120

tctattatgt gaaaggcagc ttcacccagt tttctggact ctcatgcccc catctccgac 3180

ctgggagact tcaggaatga caacctaccc agcctggtgg ggctggcagg atggtggagg 3240

tttctcaagg agctggagac ttcagggagc ccctctcatg gggaggaaag agcttccagg 3300

gggcgaacgc agcacagagg aagaggcctg ctccacttgt ctgggaacct gggcaggagg 3360

cacagaggaa gccaaggcct ggagctgcag gtcccccggc atctctctct gtcccggcag 3420

cccaggatgg cctggtgccc ccacctgctg cagcaggagc cccaaggagt gctagctgag 3480

ggtggttgct ggggtggtcc tcatggacag tgaggtgtgc aagggtgcac tgagggtggt 3540

gggaggggat cacctgggtt ccaggccatc cttgctgagc atctttgagc ctgccttccg 3600

gtgggagcag aaaaggccag accctgctga gttagaggct gctgggatcc actgtttcca 3660

cacagcggga aggctgctgg gaacaggtgg cagagaagtg ccatgtttgc gttgagcctt 3720

gcagctcttc cagctgggga ctggtgcttg ctgaaaccca ggagctgaac agtgaggagg 3780

ctgtccacct tgcttggctc actgggacca ggaaagcctg tctttggtta ggctcgtgta 3840

cttctgcagg aaaaaaaaaa aaggatgtgt cattggtcat gatatttgaa aaggggagga 3900

ggccgaagtt gttcccattt atccagtatt ggaaaatatt tgacccccct ggctgaattc 3960

ttttgcagaa ctactgtgtg tctgttcact acctttcag gtttattgtt tttatttttg 4020

catgaattaa gacgttttaa tttctttgca gacaaggtct agatgcggag tcagagatgg 4080

gactgaatgg ggagggatcc tttgtgttct catggttggc tctgactttc agctgtgttg 4140

ggaccactgg ctgatcacat cacctctctg cctcagtttc cccatctgta aaatgggaga 4200

ataatacttg cctacctacc tcacaggggt gttgtgagga ttcatttgtg attttttttt 4260

tttttgtaca gagcttttaa gcattaaaaa cagctaaatg tga 4303

<210> 52
<211> 861
<212> PRT
<213> Homo sapiens

<400> 52

Gly Cys Trp Gln Thr Met Gly Thr Thr Ala Ser Thr Ala Gln Gln Thr
1 5 10 15

Val Ser Ala Gly Thr Pro Phe Glu Gly Leu Gln Gly Ser Gly Thr Met
20 25 30

Asp Ser Arg His Ser Val Ser Ile His Ser Phe Gln Ser Thr Ser Leu

```
        35                  40                  45

His Asn Ser Lys Ala Lys Ser Ile Ile Pro Asn Lys Val Ala Pro Val
    50                  55                  60

Val Ile Thr Tyr Asn Cys Lys Glu Glu Phe Gln Ile His Asp Glu Leu
65                  70                  75                  80

Leu Lys Ala His Tyr Thr Leu Gly Arg Leu Ser Asp Asn Thr Pro Glu
                85                  90                  95

His Tyr Leu Val Gln Gly Arg Tyr Phe Leu Val Arg Asp Val Thr Glu
            100                 105                 110

Lys Met Asp Val Leu Gly Thr Val Gly Ser Cys Gly Ala Pro Asn Phe
        115                 120                 125

Arg Gln Val Gln Gly Gly Leu Thr Val Phe Gly Met Gly Gln Pro Ser
    130                 135                 140

Leu Ser Gly Phe Arg Arg Val Leu Gln Lys Leu Gln Lys Asp Gly His
145                 150                 155                 160

Arg Glu Cys Val Ile Phe Cys Val Arg Glu Glu Pro Val Leu Phe Leu
                165                 170                 175

Arg Ala Asp Glu Asp Phe Val Ser Tyr Thr Pro Arg Asp Lys Gln Asn
            180                 185                 190

Leu His Glu Asn Leu Gln Gly Leu Gly Pro Gly Val Arg Val Glu Ser
        195                 200                 205

Leu Glu Leu Ala Ile Arg Lys Glu Ile His Asp Phe Ala Gln Leu Ser
    210                 215                 220

Glu Asn Thr Tyr His Val Tyr His Asn Thr Glu Asp Leu Trp Gly Glu
225                 230                 235                 240

Pro His Ala Val Ala Ile His Gly Glu Asp Asp Leu His Val Thr Glu
                245                 250                 255

Glu Val Tyr Lys Arg Pro Leu Phe Leu Gln Pro Thr Tyr Arg Tyr His
            260                 265                 270

Arg Leu Pro Leu Pro Glu Gln Gly Ser Pro Leu Glu Ala Gln Leu Asp
        275                 280                 285
```

```
Ala Phe Val Ser Val Leu Arg Glu Thr Pro Ser Leu Leu Gln Leu Arg
    290                 295                 300

Asp Ala His Gly Pro Pro Pro Ala Leu Val Phe Ser Cys Gln Met Gly
305                 310                 315                 320

Val Gly Arg Thr Asn Leu Gly Met Val Leu Gly Thr Leu Ile Leu Leu
                325                 330                 335

His Arg Ser Gly Thr Thr Ser Gln Pro Glu Ala Ala Pro Thr Gln Ala
            340                 345                 350

Lys Pro Leu Pro Met Glu Gln Phe Gln Val Ile Gln Ser Phe Leu Arg
        355                 360                 365

Met Val Pro Gln Gly Arg Arg Met Val Glu Glu Val Asp Arg Ala Ile
    370                 375                 380

Thr Ala Cys Ala Glu Leu His Asp Leu Lys Glu Val Val Leu Glu Asn
385                 390                 395                 400

Gln Lys Lys Leu Glu Gly Ile Arg Pro Glu Ser Pro Ala Gln Gly Ser
                405                 410                 415

Gly Ser Arg His Ser Val Trp Gln Arg Ala Leu Trp Ser Leu Glu Arg
            420                 425                 430

Tyr Phe Tyr Leu Ile Leu Phe Asn Tyr Tyr Leu His Glu Gln Tyr Pro
        435                 440                 445

Leu Ala Phe Ala Leu Ser Phe Ser Arg Trp Leu Cys Ala His Pro Glu
    450                 455                 460

Leu Tyr Arg Leu Pro Val Thr Leu Ser Ser Ala Gly Pro Val Ala Pro
465                 470                 475                 480

Arg Asp Leu Ile Ala Arg Gly Ser Leu Arg Glu Asp Asp Leu Val Ser
                485                 490                 495

Pro Asp Ala Leu Ser Thr Val Arg Glu Met Asp Val Ala Asn Phe Arg
            500                 505                 510

Arg Val Pro Arg Met Pro Ile Tyr Gly Thr Ala Gln Pro Ser Ala Lys
        515                 520                 525

Ala Leu Gly Ser Ile Leu Ala Tyr Leu Thr Asp Ala Lys Arg Arg Leu
    530                 535                 540
```

```
Arg Lys Val Val Trp Val Ser Leu Arg Glu Glu Ala Val Leu Glu Cys
545                 550                 555                 560

Asp Gly His Thr Tyr Ser Leu Arg Trp Pro Gly Pro Pro Val Ala Pro
                565                 570                 575

Asp Gln Leu Glu Thr Leu Glu Ala Gln Leu Lys Ala His Leu Ser Glu
            580                 585                 590

Pro Pro Pro Gly Lys Glu Gly Pro Leu Thr Tyr Arg Phe Gln Thr Cys
        595                 600                 605

Leu Thr Met Gln Glu Val Phe Ser Gln His Arg Arg Ala Cys Pro Gly
    610                 615                 620

Leu Thr Tyr His Arg Ile Pro Met Pro Asp Phe Cys Ala Pro Arg Glu
625                 630                 635                 640

Glu Asp Phe Asp Gln Leu Leu Glu Ala Leu Arg Ala Ala Leu Ser Lys
                645                 650                 655

Asp Pro Gly Thr Gly Phe Val Phe Ser Cys Leu Ser Gly Gln Gly Arg
            660                 665                 670

Thr Thr Thr Ala Met Val Val Ala Val Leu Ala Phe Trp His Ile Gln
        675                 680                 685

Gly Phe Pro Glu Val Gly Glu Glu Glu Leu Val Ser Val Pro Asp Ala
    690                 695                 700

Lys Phe Thr Lys Gly Glu Phe Gln Val Val Met Lys Val Val Gln Leu
705                 710                 715                 720

Leu Pro Asp Gly His Arg Val Lys Lys Glu Val Asp Ala Ala Leu Asp
                725                 730                 735

Thr Val Ser Glu Thr Met Thr Pro Met His Tyr His Leu Arg Glu Ile
            740                 745                 750

Ile Ile Cys Thr Tyr Arg Gln Ala Lys Ala Ala Lys Glu Ala Gln Glu
        755                 760                 765

Met Arg Arg Leu Gln Leu Arg Ser Leu Gln Tyr Leu Glu Arg Tyr Val
    770                 775                 780

Cys Leu Ile Leu Phe Asn Ala Tyr Leu His Leu Glu Lys Ala Asp Ser
785                 790                 795                 800
```

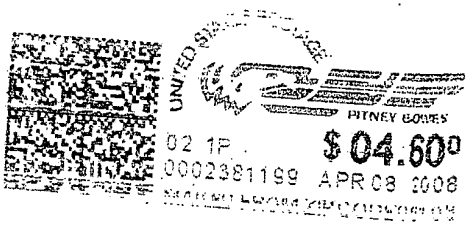
```
Trp Gln Arg Pro Phe Ser Thr Trp Met Gln Glu Val Ala Ser Lys Ala
                805                 810                 815

Gly Ile Tyr Glu Ile Leu Asn Glu Leu Gly Phe Pro Glu Leu Glu Ser
            820                 825                 830

Gly Glu Asp Gln Pro Phe Ser Arg Leu Arg Tyr Arg Trp Gln Glu Gln
        835                 840                 845

Ser Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu
    850                 855                 860
```

1



Wiggin and Dana LLP
One CityPlace
185 Asylum Street
Hartford, Connecticut
06103-3402

WIGGIN AND DANA

Counsellors at Law

MAIL STOP PCT
Commissioner for Patents
P. O. Box 1450
Alexandria, VA 22313-1450